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(21) International Application Number: PCT/US00/08399 (22) International Filing Date: 30 March 2000 (30.03.00) (30) Priority Data: 60/127,352 1 April 1999 (01.04.99) US Not furnished 1 February 2000 (01.02.00) US Not furnished 29 March 2000 (29.03.00) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Applications US 60/127,352 (CIP) Filed on 1 April 1999 (01.04.99) US Not furnished (CIP) Filed on 1 February 2000 (01.02.00) US Not furnished (CIP) Filed on 29 March 2000 (29.03.00) (71) Applicant (for all designated States except US): CURAGEN CORPORATION [US/US]; 555 Long Wharf Drive, 11th floor, New Haven, CT 06511 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): GIOT, Loic [US/US]; 3 Whalers Point, East Haven, CT 06512 (US). MANSFIELD,			Traci, A. [US/US]; 18 Manorwood, Bramford, CT 06405 (US). (74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky, and Popeo, P.C., One Financial Center, Boston, MA 02111 (US). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
(54) Title: PROTEIN-PROTEIN FROM S. CEREVISIAE AND METHODS OF USING SAME			
(57) Abstract The invention provides complexes of at least two polypeptides from the yeast <i>S. cerevisiae</i> and methods of using the same. Purified complexes of two polypeptides are provided, including chimeric complexes, and chimeric polypeptides and complexes thereof are also provided, as are nucleic acids encoding chimeric polypeptides and vectors and cells containing the same. Also provided are methods of identifying agents that disrupt polypeptide complexes, methods of identifying complex or polypeptide in a sample, and for removing the same, methods of determining altered expression of a polypeptide in a subject and methods of treating/preventing disorders involving altered levels of complex or polypeptide.			

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PROTEIN-PROTEIN FROM *S. CEREVISIAE* AND METHODS OF USING SAME

FIELD OF THE INVENTION

The invention relates generally to polypeptides and complexes of two or more
5 polypeptides, as well as to methods of use thereof.

BACKGROUND OF THE INVENTION

Most, if not all, biologically important activities are mediated at the tissue, cellular, and subcellular level at least in part by interactions between one or more proteins. These biologically important activities can include, *e.g.*, cell division, cell differentiation, anabolic
10 activities, and catabolic activities. Interacting proteins or polypeptides can form a complex. Accordingly, failure to form a given polypeptide complex can result in deleterious consequences to a cell or individual. Conversely, the inappropriate formation of a given polypeptide complex can likewise be undesirable.

The identification of protein complexes associated with specific biological activities
15 can be used to identify or prevent conditions associated with the absence or presence of these complexes.

SUMMARY OF THE INVENTION

The invention is based, in part, upon the identification of protein-protein interactions in the yeast *S. cerevisiae* and humans. Interacting proteins present in complexes according to the
20 invention are shown in, *e.g.*, Table 3.

In one aspect, the invention provides a purified complex including a first polypeptide that includes the amino acid sequence encoded by the open reading frame ("ORF") listed in Table 3, column 1, and a second polypeptide that includes the amino acid sequence of the corresponding polypeptide encoded by the ORF recited in column 5 of Table 3. Gene names
25 for the ORFs recited in Table 3, column 1, and Table 3, column 5 are provided in Table 3, columns 2 and 6, respectively.

In another aspect, the invention provides a purified complex including a first polypeptide and a second polypeptide selected from, or including, the human polypeptides

recited in Table 7, column 2, and the corresponding polypeptides recited in Table 7, column 6. Complexes of polypeptides including the binding domains of such polypeptides, and complexes having labeled polypeptide, are also provided.

The invention also provides purified complexes of a first and a second polypeptide.

5 The first polypeptide is a polypeptide functionally classified in the MIPS database as a Cell/Growth/Cell Division/DNA Synthesis protein; a Cell Rescue/Cell Defense/Cell Death and Aging Protein; a Cellular Biogenesis protein; a Cellular Organization protein; a Classification Not-Yet Clear Cut protein; an Energy Protein; an Intracellular Transport protein; an Ionic Homeostasis protein, a Metabolism protein; a Protein Destination protein; a Protein Synthesis
10 protein; a Retrotransposon/Plasmid protein; a Signal Transduction protein; a Transcription protein; a Transport Facilitation protein, or an Unclassified protein. The second polypeptide is the corresponding polypeptide recited in Table 3, column 5 or Table 7, column 6, respectively.

The invention also provides a purified complex of a first and second polypeptide, where at least one of the polypeptides is a microtubule or microtubule-associated protein, a
15 heme biosynthesis protein, or a cell wall or cell-wall synthesis protein.

The invention further provides purified chimeric complexes including a yeast polypeptide and a human ortholog polypeptide. In some embodiments the yeast polypeptide includes the amino acid sequence of the polypeptides recited in Table 7, column 1, and the human polypeptide includes the amino acid sequence of the corresponding polypeptides
20 recited in Table 7, column 6. In other embodiments the yeast polypeptide is selected from, or includes, the polypeptides recited in Table 7, column 5, and the human ortholog polypeptide is selected from, or includes, the polypeptides recited in Table 7, column 2.

In a further aspect, the invention provides chimeric polypeptides having six or more amino acids of a first polypeptide covalently linked to six or more amino acids of a second
25 polypeptide. In some embodiments, the chimeric polypeptides are yeast-yeast chimeras, while in others the chimeric polypeptides are human-human or yeast-human chimera. In some embodiments, the first polypeptide is selected from the polypeptides recited in Table 3, column 1, and the second polypeptide is selected from the polypeptides recited in Table 3, column 5. In other embodiments, the first polypeptide is selected from polypeptides recited in
30 Table 7, columns 1 or 2, and the second polypeptide is selected from the polypeptides recited in Table 7, columns 5 or 6. Nucleic acids encoding chimeric polypeptides, and vectors and cells containing the same, are also provided.

In yet another aspect, the invention provides an antibody which specifically binds polypeptide complexes according to the invention. The antibody preferably binds to a complex comprising one or more polypeptides with greater affinity than its affinity for either polypeptide that is not present in the complex.

5 Also provided by the invention are kits containing reagent which can specifically detect the complexes of the invention. In one embodiment, the reagent is a complex-specific antibody, while in other embodiments the reagent is an antibody specific for the first or second polypeptides of the complex.

10 In another aspect, the invention provides pharmaceutical compositions including the complexes described herein. Such compositions are formulated to be suitable for therapeutic administration in the treatment of deficiencies or diseases involving altered levels of the complexes of the invention.

15 In still another aspect, the invention provides methods of identifying an agent which disrupts a polypeptide complex by providing a complex described herein, contacting the complex with a test agent, and detecting the presence of a polypeptide displaced from the complex. In certain embodiments, the complex includes at least one polypeptide comprising a microtubule or microtubule-associated protein, a heme biosynthesis protein, or a cell wall or cell-wall synthesis protein.

20 In a further aspect, the invention provides a method for inhibiting the interaction of a protein with a ligand by contacting a complex of the protein and ligand with an agent that disrupts the complex. In certain embodiments, the protein is a microtubule or microtubule associated protein, a heme biosynthesis protein, or a cell wall or cell-wall synthesis protein, and the ligand is a corresponding interacting polypeptide described herein.

25 In yet another aspect, the invention provides a method of identifying a polypeptide complex in a subject by providing a biological sample from the subject and detecting, if present, the level of a complex, described herein, in the subject.

Also provided by the invention is a method for detecting a polypeptide in a biological sample by providing a biological sample containing a first polypeptide, and contacting the sample with a second polypeptide under conditions suitable to form a polypeptide complex.

30 In another aspect, the invention provides a method for removing a first polypeptide from a biological sample by providing a biological sample including the first polypeptide, contacting the sample with a second polypeptide under conditions suitable for formation of a

polypeptide complex, and removing the complex, thereby effectively removing the first polypeptide. In certain embodiments, the first polypeptide is selected from, or includes, the polypeptides recited in Table 7, column 2, and the second polypeptide is selected from, or includes, the polypeptides recited in Table 7, column 6. In another embodiment, the first
5 polypeptide is selected from, or includes, the polypeptides recited in Table 7, column 6, and the second polypeptide is selected from, or includes, the polypeptides recited in Table 7, column 2.

In a further aspect, the invention provides a method for determining altered expression of a polypeptide in a subject by providing a biological sample from the subject, measuring the
10 level of polypeptide complex in the sample, and comparing the level of the complex in the sample to the level of complex in a reference sample with a known polypeptide expression level.

In a still further aspect, the invention provides a method of treating or preventing a disease or disorder involving altered levels of a complex described herein or a polypeptide
15 described herein, by administering, to a subject in need thereof, a therapeutically-effective amount of at least one molecule that modulates the function of the complex or polypeptide. In one embodiment, the agent modulates the function of a polypeptide selected from the polypeptides recited in Table 7, columns 2 or 6.

In the specification and the appended claims, the singular forms include plural
20 referents unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. All patents and publications cited in this specification are incorporated by reference herein in their entirety.

DETAILED DESCRIPTION OF THE INVENTION

25 The invention provides complexes of interacting polypeptides which have not heretofore been shown to interact directly, as well as methods of using these complexes.

Some interacting polypeptides were identified by identifying which of the predicted open-reading frames (ORFs) of the yeast *S. cerevisiae* encode polypeptides that interact in a yeast two-hybrid system. In one screen, 692 discrete interacting protein pairs were discovered.
30 These interacting pairs include (i) interactions that place functionally unclassified proteins in a biological context, (ii) novel interactions between proteins involved in the same biological function, and (iii) novel interactions that link together biological functions into larger cellular

processes.

A summary of the screening used to identify interacting yeast ORFS is shown in Table 1.

Table 1: Screen Summary

5	Description	Total
	Yeast ORF PCR Products	6144
10	Yeast ORFs cloned ^a	5345
	ORFs pooled to generate the activation domain library	5341 ^b
	Yeast ORFs identified to have interactions ^c	817
	Total discrete interacting protein pairs	692
	Interactions identified in independent experiments ^d	286
15	Interactions identified multiple times in a single experiment	186
	Interactions identified only once	220

20 ^aNumber of PCR products giving transformants in both plasmids (pOBD2 and pOAD).

^bOne yeast ORF activation domain construct was excluded from the pool due to self-activation in a test screen (YJR009C - glyceraldehyde-3-phosphate dehydrogenase and YNL333W - Snz2) and three yeast ORF activation domain constructs were excluded because they encoded proteins that could affect the selection process (YPL248C - Gal4, YML051W - Gal80 and YEL021W - Ura3).

25 ^cThe total number of yeast ORFs found as an interacting binding domain clone and/or an interacting activation domain clone in the screens.

^dAll screening experiments were performed in duplicate.

Table 2 indicates that the interacting proteins disclosed herein can be grouped by functional roles using the Munich Information Center for Protein Sequences ("MIPS") classification system.

5 Table 2: Interactions grouped by Protein Functional Roles (as classified by the MIPS database) ^a

10 MIPS classification	MIPS Classification	Results from the screen		
	Proteins in Category ^b	Proteins with Interactions ^c	Total Interactions	Interactions within a Category
Metabolism	1023	133	189	40
Energy	239	29	39	3
15 Cell Growth, Cell Division and DNA Synthesis	767	138	227	46
Transcription	734	134	185	38
Protein Synthesis	345	18	37	5
Protein Destination	525	76	98	15
20 Transport Facilitation	302	14	20	0
Intracellular Transport	438	50	99	8
Cellular Biogenesis	185	23	35	3
Signal Transduction	122	25	32	4
Cell Rescue, Defense, Cell Death and Aging	341	48	69	7
25 Ionic Homeostasis	120	8	18	0
Cellular Organization	2144	290	388	130
Retrotransposons and Plasmid Proteins ^d	113	1	1	0
30 Classification Not Yet Clear-Cut	151	22	42	1
Unclassified Proteins	2593	313	388	110

^aIn the MIPS database, proteins have been classified into at least one category, and one third of proteins have been placed in more than one category. See MIPS Yeast Genome Database (MYGD) Functional Catalogue, www.mips.biochem.mpg.de/proj/yeast; Mewes *et al.*, *Nucl. Acid. Res.* 25: 28 (1997); Mewes *et al.*, *Nucl. Acid. Res.* 26: 33 (1998).

^bNumbers based on 6234 ORFs.

^cTotal based on 885 ORFs. Total interactions with at least one protein in the category.

40 ^dOnly eight of the yeast ORFs in this category were contained in the original 6144 ORF screening population.

Some newly disclosed interactions place functionally unclassified proteins from the yeast genome in a biological context. For example, two proteins of unknown function, YGR010Wp and YLR328Wp (77% identical), were observed to interact with each other, and also to bind to ornithine aminotransferase (Car2p), which catalyzes a step in arginine metabolism. This observation suggests that YGR010WP and YLR328Wp are implicated in arginine metabolism. In addition, because YGR010Wp and YLR328Wp are 40% identical to the human protein KIAA0479 (Genbank accession number AB007948), the interactive data further suggest tha the human protein KIAA0479 is also involved in arginine metabolism.

Also included in the interactions are complexes of two or more proteins involved in functional pathways for which direct interactions have not been described previously. For example, proteins involved in autophagy, *e.g.*, Apg13p, are shown herein to interact with proteins of the Cvt (cytoplasm-to-vacuole targeting) pathway, *e.g.*, Lap4p. Previously, direct interactions between proteins involved in autophagy and the Cvt pathway had not been reported. Autophagy is a degradation pathway used under conditions of nutrient stress to non-selectively recycle cytoplasmic proteins and organelles to their constituent components, while the Cvt pathway is a biosynthetic pathway that transports the vacuolar enzyme aminopeptidase I (API, encoded by *LAP4*) specifically to the vacuole. *See Scott et al., Curr. Opin. Cell. Biol.* 10: 523 (1998). Several mutants in the Cvt pathway (*cvt*) and autophagocytosis (*aut* and *apg*) are allelic, suggesting that both pathways utilize some of the same molecular components. *See Tsukada et al., FEBS Letters* 333: 169 (1993); Thumm *et al., FEBS Letters* 349: 275 (1994); Harding *et al., J. Cell. Biol.* 131: 17621 (1996); Scott *et al., Proc. Natl. Acad. Sci. USA* 93: 12304 (1996).

A number of ORFs encoding proteins of unknown functions have been identified as components of autophagy. Since several of the genes altered in *apg*, *aut*, and *cvt* mutants have not yet been cloned, ORFs found in these interactions can be examined to determine if they encode any of these altered genes. It has also been shown that Lap4p is a self-interactor, corroborating previous evidence that Lap4p assembles into a dodecamer (*see Funakoshi et al., Gene* 192: 207 (1997)), and the observed interaction between Apg1 and Apg13 lends support to previous genetic evidence suggesting that *APG1* is a high-copy suppressor of *apg13* (Kim *et al., J. Cell. Biol.* 137: 609 (1997)).

An interaction was also identified between YDR201Wp and YKR037Cp, two proteins known to be localized to the spindle pole body by mass spectrometry. *See Wigge et al., J. Cell Biol.* 141: 967 (1998). The interaction of these proteins may indicate their involvement in the regulation of mitotic events.

New insights into novel interactions between proteins involved in the same biological function are also provided. For example, the nuclear polyadenylated RNA-binding proteins Nab2p and Nab4p bind to the 3' end of mRNA, but have distinct roles. *See Kessler et al., Genes Dev.* 11: 2545 (1997). Nab2p is required for the regulation of poly(A) tail length and export of mRNA from the nucleus, and Nab4p is essential for the cleavage of pre-mRNA at the correct 3' site. The newly described interaction between Nab2p and Nab4p suggests that they may act in concert.

Similarly, in yeast, diverse cyclins bind to Cdc28p in a coordinated manner to modulate its kinase activity during the cell cycle. The B-type cyclins play a critical role in the induction of bipolar mitotic spindle formation. See Nasmyth, *Curr. Opin. Cell. Biol.* 5: 166 (1993). Each of the B-type cyclins, Clb1p, Clb2p and Clb3p, has presently been observed to form a complex with Cks1p and Cdc28p. The identification of interactions between Cks1p and each of Clb1p, Clb2p and Clb3p, suggests that the kinase activity of Cdc28p could be mediated by cyclin Bs through their interaction with Cks1p.

In another example, Ypt53p, a rab5-like GTPase involved in vacuolar protein sorting and endocytosis, has presently been shown to interact with Siw4p, a putative tyrosine phosphatase which acts in a complex to control nutrient-dependent cell proliferation. See Singer-Kruger *et al.*, *J. Cell. Biol.* 125: 283 (1994); Saul *et al.*, *Gen. Microbiol.* 131: 1797 (1985). One possible explanation for the observed interaction is that Ypt53p senses nutrient availability to coordinate cell cycle progression.

The newly identified protein-protein interactions connect biological functions into larger cellular processes. For example, the nuclear pore complex (NPC), consisting of as many as 50 different subunits, is the macromolecular-conducting channel between the nucleus and the cytoplasm. See Fabre *et al.*, *Ann. Rev. Genet.* 31: 277 (1997); Marelli *et al.*, *J. Cell Biol.* 143: 1813 (1998). Two newly identified NPC components, Nup53p and Nup59p/Asm4p, interact with Ndc1p, a protein required for spindle pole body (SPB) duplication and component of the nuclear envelope. Evidence of a physical interaction between components of the NPC and SPB suggests that these two structures located in the nuclear envelope may coordinate communication between the nucleus and the cytoplasm.

Another interaction involves the meiosis-specific protein, Msh5p, which is required for the resolution of cross-overs during meiosis. Hollingsworth *et al.*, *Genes Dev.* 9: 1728 (1995). Meiotic recombination is initiated by double-strand breaks (DSBs), a prerequisite to cross-over formation that is resolved in a structure called the synaptonemal complex (SC). Mre11p is part of a complex that participates in DSB formation. See Usui *et al.*, *Cell* 95: 705 (1998). It is also known that Tid3p helps form the spindle pole body and interacts with Dmc1p, a protein required for the formation of the SC. See Bishop *et al.*, *Cell* 69: 439-56 (1992). It has presently been shown that Msh5p interacts with both Mre11p and Tid3p. These novel associations tie DSB formation and the resolution of cross-overs with Msh5p as the linking protein.

Similarly, to exit the cell cycle, cells must undergo a series of checkpoints that monitor correct microtubule and spindle formation. *See Guenette et al., J. Cell. Sci. 108: 195 (1995).* The present invention identifies at least two interactions that tie cycle regulation to microtubule assembly. The first is between a microtubule checkpoint protein, Bub3p and a spindle pole body checkpoint protein, Mad3p. This observation mirrors the recent interaction described between the human homologs of Bub3p and Mad3p. *See Hoyt et al., Cell 66: 507-17 (1991); Hwang et al., Science 279: 1041 (1998); Taylor et al., J. Cell Biol. 142: 1 (1998).* Interestingly, the second is between Mad3p and a known regulator of the Cdc28p kinase, Cln3p, *See Cvrckova et al., EMBO J. 12: 5277 (1993).* These interactions could give rise to a cascade Bub3→Mad3→Cln3p→Cdc28p, and may suggest a pathway to propagate the signal of incorrect microtubule formation during early events at the cell cycle arrest in G1 phase.

The complexes disclosed herein are useful, *inter alia*, in identifying agents which modulate cellular processes in which one or more members of the complex have previously been associated. For example, interacting Pro-Pairs 1a-1b (representing open reading frames YGR108W and YBR135W, or genes CLB1 and CKS1, respectively) as shown in Table 3, have both been previously implicated in cell growth, cell division, and /or DNA synthesis. Accordingly, new agents which modulate cell growth, cell division, and/or DNA synthesis can be identified by evaluating the ability of a test agent to affect formation or dissolution of a complex of the Pro-Pairs 1a and 1b.

Complexes according to the invention can also be used in methods for identifying a desired polypeptides in a biological sample by forming a complex of a first polypeptide and a second polypeptide that interacts with the first polypeptide. The presence of the complex indicates that the sample contains the first polypeptide.

These utilities, as well as additional utilities, are discussed in greater detail below

Purified Polypeptide Complexes

In one aspect, the invention includes a purified complex that includes two or more polypeptides. In one embodiment, the invention provides purified complexes of two or more polypeptides. One of the polypeptides includes a polypeptide selected from the polypeptides recited in Table 3, column 1 (referenced as ProPair 1a-692a) and another includes a polypeptide selected from the polypeptides recited in Table 3, column 5 (referenced as ProPair 1b-692b). In some embodiments the first and second polypeptides of the complex are the

polypeptides enumerated in Table 3. In some embodiments a first polypeptide is listed as a "bait" polypeptide and a second polypeptide is denoted as "prey" polypeptide, while in other embodiments the first polypeptide corresponds to a "prey" polypeptide and the second is a "bait" polypeptide.

5 By "corresponding polypeptide" is meant, with reference to Tables 3-7, the polypeptide recited in the same row, reading across from left-to-right or right-to-left, as a specific selected peptide. For example, in Table 3, in the first row, the corresponding polypeptide of YGR108W is YBR135W. These protein pairs are designated as 1a and 1b, as is indicated in Table 3.

10 Similarly, in the first row, the corresponding polypeptide of YBR135W (ProPair 1b) is YBR108W (ProPair 1a). In the second row, however, the corresponding polypeptide of YBR135W (a prey protein; ProPair 2b) is YPR119W (a bait protein; ProPair 2a).

Also as used herein, "protein" and "protein complex" are used synonymously with "polypeptide" and "polypeptide complex." A "purified" polypeptide, protein or biologically
15 active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the polypeptide is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly
20 produced. In one embodiment, the language "substantially free of cellular material" includes preparations of polypeptide complex having less than about 30% (by dry weight) of non-complex proteins (also referred to herein as a "contaminating protein"), more preferably less than about 20% of contaminating protein, still more preferably less than about 10% of contaminating protein, and most preferably less than about 5% non-complex protein. When
25 the polypeptide or complex is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

Table 3. Protein Pairs Identified in the Screen.

Binding Domain Fusion "Bait"			Pro-Pair Functional Classification			Activation Domain Fusion "Prey"			Activation Pro-Pair Functional Classification		
Binding Domain Fusion	Domain	Ref. No. (MIPS)	Binding Domain Fusion	Domain	Ref. No. (MIPS)	Activation Domain Fusion	Domain	Ref. No. (MIPS)	Activation Domain Fusion	Domain	Ref. No. (MIPS)
[ORF]	[Gene]		[ORF]	[Gene]		[ORF]	[Gene]		[ORF]	[Gene]	
YGR108W	CLB1	1a				YBR135W	CKS1	1b			
YPR119W	CLB2	2a	Cell Growth, Cell Division And DNA Synthesis;			YBR135W	CKS1	2b	Cell Growth, Cell Division And DNA Synthesis;		
YDL155W	CLB3	3a	Cell Growth, Cell Division And DNA Synthesis;			YBR135W	CKS1	3b	Cell Growth, Cell Division And DNA Synthesis;		
YDR206W	EBS1	4a	Cell Growth, Cell Division And DNA Synthesis;			YJL030W	MAD2	4b	Cell Growth, Cell Division And DNA Synthesis;		
YDR206W	EBS1	5a	Cell Growth, Cell Division And DNA Synthesis;			YBR057C	MUM2	5b	Cell Growth, Cell Division And DNA Synthesis;		
YGL175C	SAE2	6a	Cell Growth, Cell Division And DNA Synthesis;			YGL175C	SAE2	6b	Cell Growth, Cell Division And DNA Synthesis;		
YGL229C	SAP4	7a	Cell Growth, Cell Division And DNA Synthesis;			YJL030W	MAD2	7b	Cell Growth, Cell Division And DNA Synthesis;		
YOR026W	BUB3	8a	Cell Growth, Cell Division And DNA Synthesis;			YJL013C	MAD3	8b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;		
YGL229C	SAP4	9a	Cell Growth, Cell Division And DNA Synthesis;			YJL013C	MAD3	9b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;		
YDL127W	PCL2	10a	Cell Growth, Cell Division And DNA Synthesis;			YDR146C	SWI5	10b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;		
YDR108W	GSG1	11a	Cell Growth, Cell Division And DNA Synthesis;			YGR234W	YHB1	11b	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;		
YDR099W	BMH2	12a	Cell Growth, Cell Division And DNA Synthesis;			YBL043W	ECM13	12b	Cellular Biogenesis;		
YOL034W		13a	Cell Growth, Cell Division And DNA Synthesis;			YMR117C		13b	Cellular Organization;		
YER180C	ISC10	14a	Cell Growth, Cell Division And DNA Synthesis;			YGL026C	TRP5	14b	Metabolism; Cellular Organization;		
YGL229C	SAP4	15a	Cell Growth, Cell Division And DNA Synthesis;			YBR196C	PGI1	15b	Metabolism; Energy; Cellular Organization;		
YGL158W	RCK1	16a	Cell Growth, Cell Division And DNA Synthesis;			YLR113W	HOG1	16b	Metabolism; Signal Transduction; Cell Rescue, Defense, Cell Death And Aging;		

YDR206W	EBS1	17a	Cell Growth, Cell Division And DNA Synthesis;	YER027C	GAL83	17b	Metabolism; Transcription;
YDR206W	EBS1	18a	Cell Growth, Cell Division And DNA Synthesis;	YOR047C	STD1	18b	Metabolism; Transcription;
YPR119W	CLB2	19a	Cell Growth, Cell Division And DNA Synthesis;	YNL135C	FPR1	19b	Protein Destination; Cellular Organization;
YDR206W	EBS1	20a	Cell Growth, Cell Division And DNA Synthesis;	YOL149W	DCP1	20b	Transcription;
YLR117C	SYF3	21a	DNA Synthesis;	YBR188C	NTC20	21b	Transcription;
YFL035C	MOB2	22a	Cell Growth, Cell Division And DNA Synthesis;	YOL036W		22b	Unclassified Proteins;
YDR099W	BMH2	23a	Cell Growth, Cell Division And DNA Synthesis;	YNL042W		23b	Unclassified Proteins;
YPR119W	CLB2	24a	Cell Growth, Cell Division And DNA Synthesis;	YDR386W	MUS81	24b	Unclassified Proteins;
YPR119W	CLB2	25a	Cell Growth, Cell Division And DNA Synthesis;	YDR412W		25b	Unclassified Proteins;
YPR119W	CLB2	26a	Cell Growth, Cell Division And DNA Synthesis;	YHR035W		26b	Unclassified Proteins;
YPR119W	CLB2	27a	Cell Growth, Cell Division And DNA Synthesis;	YNR022C		27b	Unclassified Proteins;
YPR046W	MCM16	28a	Cell Growth, Cell Division And DNA Synthesis;	YJR135C	MCM22	28b	Unclassified Proteins;
YOR127W	RGA1	29a	Cell Growth, Cell Division And DNA Synthesis;	YHL042W		29b	Unclassified Proteins;
YOR127W	RGA1	30a	Cell Growth, Cell Division And DNA Synthesis;	YJL185C		30b	Unclassified Proteins;
YGL175C	SAE2	31a	Cell Growth, Cell Division And DNA Synthesis;	YCR086W		31b	Unclassified Proteins;
YGL229C	SAP4	32a	Cell Growth, Cell Division And DNA Synthesis;	YJL178C		32b	Unclassified Proteins;
YGL229C	SAP4	33a	Cell Growth, Cell Division And DNA Synthesis;	YJL211C		33b	Unclassified Proteins;
YGL229C	SAP4	34a	Cell Growth, Cell Division And DNA Synthesis;	YMR181C		34b	Unclassified Proteins;
YGL229C	SAP4	35a	Cell Growth, Cell Division And DNA Synthesis;	YOR062C		35b	Unclassified Proteins;
YGL229C	SAP4	36a	Cell Growth, Cell Division And DNA Synthesis;	YPR040W		36b	Unclassified Proteins;
YMR096W	SNZ1	37a	Cell Growth, Cell Division And DNA Synthesis;	YMR095C	SNO1	37b	Unclassified Proteins;
YHR014W	SPO13	38a	Cell Growth, Cell Division And DNA Synthesis;	YHR185C		38b	Unclassified Proteins;
YLR215C		39a	Cell Growth, Cell Division And DNA Synthesis;	YLR386W		39b	Unclassified Proteins;

YDR076W	RAD55	40a	Cell Growth, Cell Division And DNA Synthesis; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YER095W	RAD51	40b	Cell Growth, Cell Division And DNA Synthesis; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YOR368W	RAD17	41a	Cell Growth, Cell Division And DNA Synthesis; Cell Rescue, Defense, Cell Death And Aging;	YLR288C	MEC3	41b	Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Cell Rescue, Defense, Cell Death And Aging; Unclassified Proteins;
YPL204W	HRR25	42a	Cell Growth, Cell Division And DNA Synthesis; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YHR185C		42b	Unclassified Proteins;
YJL160C		43a	Cell Growth, Cell Division And DNA Synthesis; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YCR059C		43b	Unclassified Proteins;
YPL140C	MKK2	44a	Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Signal Transduction; Cell Rescue, Defense, Cell Death And Aging;	YHR030C	SLT2	44b	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction; Cell Rescue, Defense, Cell Death And Aging;
YLR288C	MEC3	45a	Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Cell Rescue, Defense, Cell Death And Aging;	YMR159C	SAP18	45b	Unclassified Proteins;
YGR014W	MSB2	46a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YJL030W	MAD2	46b	Cell Growth, Cell Division And DNA Synthesis;
YDL154W	MSH5	47a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YBR133C	HSL7	47b	Cell Growth, Cell Division And DNA Synthesis;
YDL154W	MSH5	48a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YMR224C	MRE11	48b	Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YAL040C	CLN3	49a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YJL013C	MAD3	49b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YPL049C	DIG1	50a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YDR480W	DIG2	50b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YER179W	DMC1	51a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YER179W	DMC1	51b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YIL150C	DNA43	52a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YGL201C	MCM6	52b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;

YGR014W	MSB2	53a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YJL013C	MAD3	53b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YHR184W	SSP1	54a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YHR184W	SSP1	54b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YDR388W	RVS167	55a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YCR009C	RVS161	55b	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;
YGR014W	MSB2	56a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YDL165W	CDC36	56b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YDL154W	MSH5	57a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YGL025C	PGD1	57b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YMR139W	RIM11	58a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YJR094C	IME1	58b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YML031W	NDC1	59a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YDL088C	ASM4	59b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YDL017W	CDC7	60a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YGR099W	TEL2	60b	Cellular Organization;
YGR014W	MSB2	61a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YIL144W	TID3	61b	Cellular Organization;
YDL154W	MSH5	62a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YIL144W	TID3	62b	Cellular Organization;
YDL017W	CDC7	63a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YKL039W	PTM1	63b	Classification Not Yet Clear-Cut;
YOL069W	NUF2	64a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YER099C	PRS2	64b	Metabolism;
YDR218C	SPR28	65a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YJR076C	CDC11	65b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YDL017W	CDC7	66a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YJL088W	ARG3	66b	Metabolism; Cellular Organization;
YDL017W	CDC7	67a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YDL160C	DHH1	67b	Transcription; Cellular Organization;
YGR014W	MSB2	68a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YPL211W	NIP7	68b	Transcription; Cellular Organization;

YLR319C	BUD6	69a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YGL015C	69b	Unclassified Proteins;
YDL017W	CDC7	70a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YCR022C	70b	Unclassified Proteins;
YDL017W	CDC7	71a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YCR050C	71b	Unclassified Proteins;
YDL017W	CDC7	72a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YEL023C	72b	Unclassified Proteins;
YDL017W	CDC7	73a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YFR057W	73b	Unclassified Proteins;
YDL017W	CDC7	74a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YNR048W	74b	Unclassified Proteins;
YDL017W	CDC7	75a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YOR006C	75b	Unclassified Proteins;
YDL154W	MSH5	76a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YGL170C	76b	Unclassified Proteins;
YML031W	NDC1	77a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YMR153W	77b	Unclassified Proteins;
YNL189W	SRP1	78a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YKL130C	78b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YDR335W	MSN5	79a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport;	YDR146C	79b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YNL189W	SRP1	80a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YML028W	80b	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YNL189W	SRP1	81a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YMR226C	81b	Classification Not Yet Clear-Cut;
YNL154C	YCK2	82a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YOR355W	82b	Classification Not Yet Clear-Cut;
YNL189W	SRP1	83a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YBR252W	83b	Metabolism;

YNL189W	SRP1	84a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YPR062W	FCY1	84b	Metabolism;
YNL189W	SRP1	85a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YJR159W	SOR1	85b	Metabolism;
YNL189W	SRP1	86a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YPL214C	THI6	86b	Metabolism;
YNL189W	SRP1	87a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YFL061W		87b	Metabolism;
YNL189W	SRP1	88a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YOL058W	ARG1	88b	Metabolism; Cellular Organization;
YNL189W	SRP1	89a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YPL111W	CAR1	89b	Metabolism; Cellular Organization;
YNL189W	SRP1	90a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YLR303W	MET17	90b	Metabolism; Cellular Organization;
YNL189W	SRP1	91a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YDL236W	PHO13	91b	Metabolism; Cellular Organization;
YNL189W	SRP1	92a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YER065C	ICL1	92b	Metabolism; Energy; Cellular Organization;
YNL154C	YCK2	93a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YMR267W	PPA2	93b	Metabolism; Energy; Cellular Organization;
YNL189W	SRP1	94a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YGL221C	NIF3	94b	Transcription;
YNL189W	SRP1	95a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YHL009C	YAP3	95b	Transcription; Cellular Organization;
YNL154C	YCK2	96a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YCL054W		96b	Transcription; Cellular Organization;
YNL154C	YCK2	97a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YCR011C	ADP1	97b	Transport Facilitation; Cellular Organization;

YCR009C	RVS161	98a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YBR108W	98b	Unclassified Proteins;
YNL189W	SRP1	99a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YJR133W	99b	Unclassified Proteins;
YNL189W	SRP1	100a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YGR024C	100b	Unclassified Proteins;
YNL154C	YCK2	101a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YER079W	101b	Unclassified Proteins;
YNL154C	YCK2	102a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YKL204W	102b	Unclassified Proteins;
YNL154C	YCK2	103a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YMR180C	103b	Unclassified Proteins;
YGL116W	CDC20	104a	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;	YJL030W	104b	Cell Growth, Cell Division And DNA Synthesis;
YJL001W	PRE3	105a	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YLR386W	105b	Unclassified Proteins;
YFR052W	RPN12	106a	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YDR273W	106b	Unclassified Proteins;
YFR052W	RPN12	107a	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YJR133W	107b	Unclassified Proteins;
YBL105C	PKC1	108a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YML109W	108b	Cell Growth, Cell Division And DNA Synthesis;

YPR054W	SMK1	109a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;	YFL029C	CAK1	109b	Cell Growth, Cell Division And DNA Synthesis;
YLR229C	CDC42	110a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction; Cellular Organization;	YDL135C	RD11	110b	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction; Cellular Organization;
YLR362W	STE11	111a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;	YCL032W	STE50	111b	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;
YJR086W	STE18	112a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction; Cellular Organization;	YOR212W	STE4	112b	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction; Cellular Organization;
YLR305C	STT4	113a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;	YOR355W	GDS1	113b	Classification Not Yet Clear-Cut;
YLR305C	STT4	114a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;	YOR047C	STD1	114b	Metabolism; Transcription;
YMR052W	FAR3	115a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;	YFR008W		115b	Unclassified Proteins;
YAR003W		116a	Cell Growth, Cell Division And DNA Synthesis; Transcription;	YBR175W		116b	Unclassified Proteins;
YAR003W		117a	Cell Growth, Cell Division And DNA Synthesis; Transcription;	YDR140W		117b	Unclassified Proteins;
YGL192W	IME4	118a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YBR057C	MUM2	118b	Cell Growth, Cell Division And DNA Synthesis;
YCL055W	KAR4	119a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YBR057C	MUM2	119b	Cell Growth, Cell Division And DNA Synthesis;
YNL210W	MER1	120a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YKL142W	MRP8	120b	Protein Synthesis; Cellular Organization;
YOR061W	CKA2	121a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YOR039W	CKB2	121b	Transcription; Cellular Organization;
YNR010W	CSE2	122a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YOR174W	MED4	122b	Transcription; Cellular Organization;
YHL027W	RIM101	123a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YJL056C	ZAP1	123b	Transcription; Cellular Organization;
YOL006C	TOP1	124a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YMR233W		124b	Unclassified Proteins;

YLR433C	CNA1	125a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Ionic Homeostasis; Cellular Organization;	YNL047C	125b	Unclassified Proteins;
YGL058W	RAD6	126a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Protein Destination; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YCR066W RAD18	126b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YPR018W	RLF2	127a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Protein Destination; Cellular Organization;	YBR195C MS11	127b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Protein Destination; Cellular Biogenesis; Signal Transduction; Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YHR084W	STE12	128a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Signal Transduction; Cellular Organization;	YDR480W DIG2	128b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YBR244W		129a	Cell Rescue, Defense, Cell Death And Aging;	YLR117C SYF3	129b	Cell Growth, Cell Division And DNA Synthesis;
YLL057C		130a	Cell Rescue, Defense, Cell Death And Aging;	YLL057C	130b	Cell Rescue, Defense, Cell Death And Aging;
YIL011W		131a	Cell Rescue, Defense, Cell Death And Aging;	YMR201C RAD14	131b	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YHL046C		132a	Cell Rescue, Defense, Cell Death And Aging;	YOR355W GDS1	132b	Classification Not Yet Clear-Cut;
YGR213C	RTA1	133a	Cell Rescue, Defense, Cell Death And Aging;	YHR134W	133b	Unclassified Proteins;
YDR061W		134a	Cell Rescue, Defense, Cell Death And Aging;	YCR086W	134b	Unclassified Proteins;
YLR046C		135a	Cell Rescue, Defense, Cell Death And Aging;	YHL006C	135b	Unclassified Proteins;
YJL092W	HPR5	136a	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YOR355W GDS1	136b	Classification Not Yet Clear-Cut;
YDR077W	SED1	137a	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YDR044W HEM13	137b	Metabolism; Cellular Organization;
YJL092W	HPR5	138a	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YDR510W SMT3	138b	Protein Destination;
YJL092W	HPR5	139a	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YBR184W MEL1	139b	Unclassified Proteins;
YJL092W	HPR5	140a	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YDR078C PUN1	140b	Unclassified Proteins;
YLR390W	ECM19	141a	Cellular Biogenesis;	YDR145W TAF61	141b	Transcription;
YHR171W		142a	Cellular Biogenesis; Cellular Organization;	YBR217W	142b	Protein Destination; Cellular Biogenesis; Cellular Organization;
YHR171W		143a	Cellular Biogenesis; Cellular Organization;	YNR007C AUT1	143b	Protein Destination; Intracellular Transport;

YHR171W	144a	Cellular Biogenesis; Cellular Organization;	YBL078C	AUT7	144b	Protein Destination; Intracellular Transport; Cellular Organization;
YKR037C	145a	Cellular Organization;	YJR091C	JSN1	145b	Cell Growth, Cell Division And DNA Synthesis;
YCL059C	146a	Cellular Organization;	YGL201C	MCM6	146b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YOR106W	147a	Cellular Organization;	YHR129C	ARP1	147b	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;
YMR092C	148a	Cellular Organization;	YLR102C	APC9	148b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination;
YDR201W	149a	Cellular Organization;	YIL144W	TID3	149b	Cellular Organization;
YER018C	150a	Cellular Organization;	YMR117C		150b	Cellular Organization;
YKR037C	151a	Cellular Organization;	YDR201W		151b	Cellular Organization;
YLR429W	152a	Cellular Organization;	YDR328C	SKP1	152b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;
YER018C	153a	Cellular Organization;	YHR193C	EGD2	153b	Metabolism; Transcription; Cellular Organization;
YDR122W	154a	Cellular Organization;	YOL082W		154b	Unclassified Proteins;
YNL218W	155a	Classification Not Yet Clear-Cut;	YJL030W	MAD2	155b	Cell Growth, Cell Division And DNA Synthesis;
YNL023C	156a	Classification Not Yet Clear-Cut;	YMR224C	MRE11	156b	Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YNL023C	157a	Classification Not Yet Clear-Cut;	YKL130C	SHE2	157b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;
YCL024W	158a	Classification Not Yet Clear-Cut;	YKR048C	NAP1	158b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Biogenesis; Cellular Organization;
YFR024C-A	159a	Classification Not Yet Clear-Cut;	YBL007C	SLA1	159b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;
YNL218W	160a	Classification Not Yet Clear-Cut;	YNL218W		160b	Classification Not Yet Clear-Cut;
YLL046C	161a	Classification Not Yet Clear-Cut;	YFR047C		161b	Metabolism;
YBR274W	162a	Classification Not Yet Clear-Cut;	YLR258W	GSY2	162b	Metabolism; Energy; Cellular Organization;
YDL002C	163a	Classification Not Yet Clear-Cut;	YER092W		163b	Unclassified Proteins;
YER059W	164a	Classification Not Yet Clear-Cut;	YJL084C		164b	Unclassified Proteins;

YER059W	PCL6	165a	Classification Not Yet Clear-Cut;	YLR190W	165b	Unclassified Proteins;
YBR274W		166a	Classification Not Yet Clear-Cut;	YMR255W	166b	Unclassified Proteins;
YDR084C		167a	Classification Not Yet Clear-Cut;	YGL161C	167b	Unclassified Proteins;
YDR084C		168a	Classification Not Yet Clear-Cut;	YGL198W	168b	Unclassified Proteins;
YFR024C-A		169a	Classification Not Yet Clear-Cut;	YGR268C	169b	Unclassified Proteins;
YMR077C		170a	Classification Not Yet Clear-Cut;	YKL052C	170b	Unclassified Proteins;
YHR039C		171a	Energy;	YDR480W	DIG2	Cell Growth, Cell Division And
					171b	DNA Synthesis; Cellular
						Organization;
YPR048W		172a	Energy;	YOR355W	GDS1	Classification Not Yet Clear-Cut;
YPR048W		173a	Energy;	YDL215C	GDH2	Metabolism; Cellular
						Organization;
YPR048W		174a	Energy;	YNL199C	GCR2	Metabolism; Transcription;
						Cellular Organization;
YNL118C	PSU1	175a	Energy;	YOL149W	DCP1	Transcription;
YNL118C	PSU1	176a	Energy;	YEL015W		Unclassified Proteins;
YPR048W		177a	Energy;	YPR070W		Unclassified Proteins;
YPL174C	NIP100	178a	Intracellular Transport;	YHR129C	ARP1	Cell Growth, Cell Division And
						DNA Synthesis; Intracellular
						Transport; Cellular Organization;
YPL174C	NIP100	179a	Intracellular Transport;	YIL144W	TID3	Cellular Organization;
YGR057C	LST7	180a	Intracellular Transport;	YKL015W	PUT3	Metabolism; Transcription;
						Cellular Organization;
YPL174C	NIP100	181a	Intracellular Transport;	YJL184W		Unclassified Proteins;
YER105C	NUP157	182a	Intracellular Transport; Cellular	YJL030W	MAD2	Cell Growth, Cell Division And
			Organization;			DNA Synthesis;
YFR002W	NIC96	183a	Intracellular Transport; Cellular	YGR120C		Intracellular Transport; Cellular
			Organization;			Organization;
YHL019C	APM2	184a	Intracellular Transport; Cellular	YKL135C	APL2	Protein Destination; Intracellular
			Organization;			Transport; Cellular Organization;
YGR119C	NUP57	185a	Intracellular Transport; Cellular	YMR236W	TAF17	Transcription; Cellular
			Organization;			Organization;
YGR119C	NUP57	186a	Intracellular Transport; Cellular	YJL041W	NSP1	Transcription; Intracellular
			Organization;			Transport; Cellular Organization;
YGR119C	NUP57	187a	Intracellular Transport; Cellular	YGL172W	NUP49	Transcription; Intracellular
			Organization;			Transport; Cellular Organization;
YFR002W	NIC96	188a	Intracellular Transport; Cellular	YMR153W		Unclassified Proteins;
			Organization;			
YER105C	NUP157	189a	Intracellular Transport; Cellular	YEL015W		Unclassified Proteins;
			Organization;			
YER105C	NUP157	190a	Intracellular Transport; Cellular	YMR153W		Unclassified Proteins;
			Organization;			
YMR129W	POM152	191a	Intracellular Transport; Cellular	YJL057C	IKS1	Unclassified Proteins;
			Organization;			
YMR129W	POM152	192a	Intracellular Transport; Cellular	YMR153W		Unclassified Proteins;
			Organization;			
YNL287W	SEC21	193a	Intracellular Transport; Cellular	YBR281C		Unclassified Proteins;
			Organization;			

YOR115C	194a	Intracellular Transport; Cellular Organization;	YOL082W	194b	Unclassified Proteins;
YDR503C	195a	Metabolism;	YKL130C	195b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YOR128C	196a	Metabolism;	YCR066W	196b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YNL201C	197a	Metabolism;	YOR355W	197b	Classification Not Yet Clear-Cut;
YOR128C	198a	Metabolism;	YCR067C	198b	Intracellular Transport; Cellular Organization;
YOR128C	199a	Metabolism;	YOR128C	199b	Metabolism;
YIR032C	200a	Metabolism;	YIR032C	200b	Metabolism;
YGR267C	201a	Metabolism;	YGR267C	201b	Metabolism;
YOL061W	202a	Metabolism;	YER099C	202b	Metabolism;
YPL214C	203a	Metabolism;	YPL214C	203b	Metabolism;
YNR012W	204a	Metabolism;	YDR020C	204b	Metabolism;
YDL246C	205a	Metabolism;	YJR159W	205b	Metabolism;
YDL246C	206a	Metabolism;	YDL246C	206b	Metabolism;
YFR047C	207a	Metabolism;	YFR047C	207b	Metabolism;
YHL018W	208a	Metabolism;	YHL018W	208b	Metabolism;
YHR111W	209a	Metabolism;	YHR111W	209b	Metabolism;
YIL074C	210a	Metabolism;	YER081W	210b	Metabolism;
YIL074C	211a	Metabolism;	YIL074C	211b	Metabolism;
YLR245C	212a	Metabolism;	YLR245C	212b	Metabolism;
YLR432W	213a	Metabolism;	YDL215C	213b	Metabolism; Cellular Organization;
YNL201C	214a	Metabolism;	YFL056C	214b	Metabolism; Energy;
YOR226C	215a	Metabolism;	YPL088W	215b	Metabolism; Energy;
YNL201C	216a	Metabolism;	YOR047C	216b	Metabolism; Transcription;
YDL013W	217a	Metabolism;	YDR510W	217b	Protein Destination;
YLR432W	218a	Metabolism;	YKR026C	218b	Protein Synthesis; Cellular Organization;
YHR204W	219a	Metabolism;	YGL030W	219b	Protein Synthesis; Cellular Organization;
YBR006W	220a	Metabolism;	YDR382W	220b	Protein Synthesis; Cellular Organization;
YDL013W	221a	Metabolism;	YER116C	221b	Transcription;
YNL201C	222a	Metabolism;	YPR115W	222b	Transcription;
YPL059W	223a	Metabolism;	YIL105C	223b	Transcription;
YLR432W	224a	Metabolism;	YDR167W	224b	Transcription; Cellular Organization;
YOR128C	225a	Metabolism;	YBR134W	225b	Unclassified Proteins;
YGR155W	226a	Metabolism;	YCR086W	226b	Unclassified Proteins;
YOR269W	227a	Metabolism;	YLR254C	227b	Unclassified Proteins;
YBR006W	228a	Metabolism;	YKL023W	228b	Unclassified Proteins;

YDL203C	229a	Metabolism;	YGR058W	229b	Unclassified Proteins;
YDL203C	230a	Metabolism;	YOR372C	230b	Unclassified Proteins;
YDR400W	231a	Metabolism;	YCR059C	231b	Unclassified Proteins;
YHR204W	232a	Metabolism;	YER126C	232b	Unclassified Proteins;
YLR432W	233a	Metabolism;	YDR469W	233b	Unclassified Proteins;
YPL059W	234a	Metabolism;	YNL047C	234b	Unclassified Proteins;
YDL006W	235a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Signal Transduction; Cell Rescue, Defense, Cell Death And Aging; Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;	YDR162C	235b	Protein Destination;
YDR328C	SKP1	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;	YFL009W	CDC4	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YGL155W	CDC43	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;	YKL019W	RAM2	Metabolism; Protein Destination; Cellular Organization;
YDR328C	SKP1	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;	YLR352W		Unclassified Proteins;
YPL161C	BEM4	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;	YGL126W	SCS3	Metabolism;
YPL161C	BEM4	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;	YIL163C		Unclassified Proteins;
YPL161C	BEM4	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;	YLR049C		Unclassified Proteins;
YNL236W	SIN4	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YJL030W	MAD2	Cell Growth, Cell Division And DNA Synthesis;
YNL236W	SIN4	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YGL238W	CSE1	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YNL236W	SIN4	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YJL013C	MAD3	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YNL236W	SIN4	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YOR355W	GDS1	Classification Not Yet Clear-Cut;

YDR207C	UME6	246a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YOR355W	GDS1	246b	Classification Not Yet Clear-Cut;
YNL236W	SIN4	247a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YFR033C	QCR6	247b	Energy; Cellular Organization;
YNL236W	SIN4	248a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YJR034W	PET191	248b	Energy; Protein Destination; Cellular Organization;
YNL236W	SIN4	249a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YDR054C	CDC34	249b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;
YNL236W	SIN4	250a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YKL012W	PRP40	250b	Transcription; Cellular Organization;
YNL236W	SIN4	251a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YGR046W		251b	Unclassified Proteins;
YNL236W	SIN4	252a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YGR117C		252b	Unclassified Proteins;
YDR207C	UME6	253a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YOL082W		253b	Unclassified Proteins;
YGR144W	THI4	254a	Metabolism; Cell Rescue, Defense, Cell Death And Aging;	YGR144W	THI4	254b	Metabolism; Cell Rescue, Defense, Cell Death And Aging;
YER062C	HOR2	255a	Metabolism; Cell Rescue, Defense, Cell Death And Aging;	YPL201C		255b	Unclassified Proteins;
YDR477W	SNF1	256a	Metabolism; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YER027C	GAL83	256b	Metabolism; Transcription;
YBR176W	ECM31	257a	Metabolism; Cellular Biogenesis;	YBR176W	ECM31	257b	Metabolism; Cellular Biogenesis;
YDR376W	ARH1	258a	Metabolism; Cellular Organization;	YIR024C	GIF1	258b	Cell Growth, Cell Division And DNA Synthesis;
YDR408C	ADE8		Metabolism; Cellular Organization;	YGL127C	SOH1		Cell Growth, Cell Division And DNA Synthesis; Transcription;
YDR376W	ARH1	259a	Metabolism; Cellular Organization;	YCR093W	CDC39	259b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YDR408C	ADE8	260a	Metabolism; Cellular Organization;	YCR063W		260b	Classification Not Yet Clear-Cut;

YLR438W	CAR2	261a	Metabolism; Cellular Organization;	YHL025W	SNF6	261b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YOR180C	EHD2	262a	Metabolism; Cellular Organization;	YLR284C	EHD1	262b	Metabolism; Cellular Organization;
YOR202W	HIS3	263a	Metabolism; Cellular Organization;	YOR202W	HIS3	263b	Metabolism; Cellular Organization;
YER023W	PRO3	264a	Metabolism; Cellular Organization;	YER023W	PRO3	264b	Metabolism; Cellular Organization;
YKL067W	YNK1	265a	Metabolism; Cellular Organization;	YKL067W	YNK1	265b	Metabolism; Cellular Organization;
YGL154C	LYS5	266a	Metabolism; Cellular Organization;	YGL254W	FZF1	266b	Metabolism; Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YGR229C	SMI1	267a	Metabolism; Cellular Organization;	YKR099W	BAS1	267b	Metabolism; Transcription; Cellular Organization;
YBL042C	FUI1	268a	Metabolism; Cellular Organization;	YER021W	RPN3	268b	Protein Destination;
YHR128W	FUR1	269a	Metabolism; Cellular Organization;	YPR185W	APG13	269b	Protein Destination; Intracellular Transport;
YOR375C	GDH1	270a	Metabolism; Cellular Organization;	YJL124C	SPB8	270b	Transcription;
YDR408C	ADE8	271a	Metabolism; Cellular Organization;	YOR174W	MED4	271b	Transcription; Cellular Organization;
YOR303W	CPA1	272a	Metabolism; Cellular Organization;	YOR039W	CKB2	272b	Transcription; Cellular Organization;
YGR061C	ADE6	273a	Metabolism; Cellular Organization;	YLR386W		273b	Unclassified Proteins;
YLR438W	CAR2	274a	Metabolism; Cellular Organization;	YGR010W		274b	Unclassified Proteins;
YLR438W	CAR2	275a	Metabolism; Cellular Organization;	YLR328W		275b	Unclassified Proteins;
YOL059W	GPD2	276a	Metabolism; Cellular Organization;	YFL017C		276b	Unclassified Proteins;
YNL104C	LEU4	277a	Metabolism; Cellular Organization;	YKL183W		277b	Unclassified Proteins;
YLR345W		278a	Metabolism; Energy;	YLR321C	SFH1	278b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Biogenesis; Cellular Organization;
YJL137C	GLG2	279a	Metabolism; Energy;	YJL137C	GLG2	279b	Metabolism; Energy;
YGL134W	PCL10	280a	Metabolism; Energy;	YPL031C	PHO85	280b	Metabolism; Energy; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YLR345W		281a	Metabolism; Energy;	YGR158C	MTR3	281b	Transcription; Cellular Organization;
YKR096W		282a	Metabolism; Energy;	YBL051C		282b	Unclassified Proteins;
YER133W	GLC7	283a	Metabolism; Energy; Cell Division And DNA Synthesis; Protein Synthesis; Cellular Organization;	YNL233W	BNI4	283b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;

YLR071C	RGR1	284a	Metabolism; Energy; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YDL065C	PEX19	284b	Cellular Organization;
YDR074W	TPS2	285a	Metabolism; Energy; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YER019C-A SBH2		285b	Protein Destination; Transport Facilitation; Intracellular Transport;
YDR074W	TPS2	286a	Metabolism; Energy; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YAR066W		286b	Unclassified Proteins;
YBR221C	POB1	287a	Metabolism; Energy; Cellular Organization;	YLR345W		287b	Metabolism; Energy;
YDR148C	KGD2	288a	Metabolism; Energy; Cellular Organization;	YDR510W SMT3		288b	Protein Destination;
YMR267W	PPA2	289a	Metabolism; Energy; Cellular Organization;	YKR026C GCN3		289b	Protein Synthesis; Cellular Organization;
YDR001C		290a	Metabolism; Energy; Cellular Organization;	YLR270W		290b	Unclassified Proteins;
YCL040W	GLK1	291a	Metabolism; Energy; Intracellular Transport; Cellular Organization;	YBR040W FIG1		291b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YCL040W	GLK1	292a	Metabolism; Energy; Intracellular Transport; Cellular Organization;	YML099C ARG81		292b	Metabolism; Transcription; Cellular Organization;
YMR079W	SEC14	293a	Metabolism; Intracellular Transport; Cellular Organization;	YDL001W		293b	Unclassified Proteins;
YDL090C	RAM1	294a	Metabolism; Protein Destination; Signal Transduction; Cellular Organization;	YKL019W RAM2		294b	Metabolism; Protein Destination; Cellular Organization;
YLR150W	STM1	295a	Metabolism; Signal Transduction;	YJR072C		295b	Unclassified Proteins;
YGL254W	FZF1	296a	Metabolism; Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YHR215W PHO12		296b	Metabolism; Cellular Organization;
YGL115W	SNF4	297a	Metabolism; Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YER027C GAL83		297b	Metabolism; Transcription;
YGL254W	FZF1	298a	Metabolism; Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YOR039W CKB2		298b	Transcription; Cellular Organization;
YGL254W	FZF1	299a	Metabolism; Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YGR047C TFC4		299b	Transcription; Cellular Organization;
YOL108C	INO4	300a	Metabolism; Transcription; Cellular Organization;	YKL017C HCS1		300b	Cell Growth, Cell Division And DNA Synthesis;
YOL108C	INO4	301a	Metabolism; Transcription; Cellular Organization;	YMR317W		301b	Cellular Biogenesis;
YNL314W	DAL82	302a	Metabolism; Transcription; Cellular Organization;	YNL314W DAL82		302b	Metabolism; Transcription; Cellular Organization;
YOL108C	INO4	303a	Metabolism; Transcription;	YDR123C INO2		303b	Metabolism; Transcription;

YOL108C	INO4	304a	Cellular Organization; Metabolism; Transcription;	YKL135C	APL2	304b	Cellular Organization; Protein Destination; Intracellular Transport; Cellular Organization;
YJL110C	GZF3	305a	Cellular Organization; Metabolism; Transcription;	YNL021W	HDA1	305b	Transcription; Protein Destination; Cellular Organization;
YOL108C	INO4	306a	Metabolism; Transcription; Cellular Organization;	YNL279W		306b	Unclassified Proteins;
YOR348C	PUT4	307a	Metabolism; Transcription; Intracellular Transport; Cellular Organization;	YMR228W	MTF1	307b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YOR348C	PUT4	308a	Metabolism; Transcription; Intracellular Transport; Cellular Organization;	YCR045C		308b	Protein Destination;
YOR348C	PUT4	309a	Metabolism; Transcription; Intracellular Transport; Cellular Organization;	YJL084C		309b	Unclassified Proteins;
YOR348C	PUT4	310a	Metabolism; Transcription; Intracellular Transport; Cellular Organization;	YLR294C		310b	Unclassified Proteins;
YMR091C	NPL6	311a	Protein Destination;	YFR037C	RSC8	311b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YER144C	UBP5	312a	Protein Destination;	YBR059C		312b	Classification Not Yet Clear-Cut; Metabolism;
YLR417W	VPS36	313a	Protein Destination;	YPL002C	SNF8	313b	Metabolism; Transcription;
YDL097C	RPN6	314a	Protein Destination;	YEL009C	GCN4	314b	Cellular Organization;
YDR394W	RPT3	315a	Protein Destination;	YGR232W		315b	Protein Destination;
YPL003W	ULA1	316a	Protein Destination;	YPR066W	UBA3	316b	Protein Destination;
YOR132W	VPS17	317a	Protein Destination;	YOR069W	VPS5	317b	Organization; Transcription; Ionic Homeostasis;
YDR098C		318a	Protein Destination;	YGL071W	RCS1	318b	Cellular Organization;
YER174C		319a	Protein Destination;	YGL071W	RCS1	319b	Transcription; Ionic Homeostasis;
YML094W	GIM5	320a	Protein Destination;	YLR200W	YKE2	320b	Cellular Organization;
YOL111C		321a	Protein Destination;	YOR007C	SGT2	321b	Unclassified Proteins;
YHR057C	CYP2	322a	Protein Destination; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YJR091C	JSN1	322b	Cell Growth, Cell Division And DNA Synthesis;
YPL149W	APG5	323a	Protein Destination; Cellular Biogenesis; Cellular Organization;	YBR217W		323b	Protein Destination; Cellular Biogenesis; Cellular Organization;
YPL149W	APG5	324a	Protein Destination; Cellular Biogenesis; Cellular Organization;	YMR159C	SAP18	324b	Unclassified Proteins;
YBR217W		325a	Protein Destination; Cellular Biogenesis; Cellular Organization;	YMR159C	SAP18	325b	Unclassified Proteins;

YMR314W	PRES	326a	Protein Destination; Cellular Organization;	YKL130C	SHE2	326b	Cell Growth, Cell Division And DNA Synthesis; Cellular Energy;
YPR051W	MAK3	327a	Protein Destination; Cellular Organization;	YEL053C	MAK10	327b	
YNL135C	FPR1	328a	Protein Destination; Cellular Organization;	YER052C	HOM3	328b	Metabolism;
YKL103C	LAP4	329a	Protein Destination; Cellular Organization;	YKL103C	LAP4	329b	Protein Destination; Cellular Organization;
YHR060W	VMA22	330a	Protein Destination; Cellular Organization;	YLR447C	VMA6	330b	Protein Destination; Transport Facilitation; Intracellular Transport; Ionic Homeostasis; Cellular Organization; Protein Synthesis; Cellular Organization; Unclassified Proteins;
YOL088C	MPD2	331a	Protein Destination; Cellular Organization;	YHR091C	MSR1	331a	Unclassified Proteins;
YKL103C	LAP4	332a	Protein Destination; Cellular Organization;	YOL082W		332b	Unclassified Proteins;
YOL088C	MPD2	333a	Protein Destination; Cellular Organization;	YLR312C		333b	Unclassified Proteins;
YEL060C	PRB1	334a	Protein Destination; Cellular Organization;	YML032C-A		334b	Unclassified Proteins;
YOR362C	PRE10	335a	Protein Destination; Cellular Organization;	YFL017C		335b	Unclassified Proteins;
YDR292C	SRP101	336a	Protein Destination; Cellular Organization;	YMR163C		336b	Unclassified Proteins;
YHR060W	VMA22	337a	Protein Destination; Cellular Organization;	YDR469W		337b	Unclassified Proteins;
YPR185W	APG13	338a	Protein Destination; Intracellular Transport;	YGL180W	APG1	338b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Intracellular Transport; Cellular Organization; Cell Growth; Cell Division And DNA Synthesis; Protein Destination; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization; Intracellular Transport; Cellular Organization; Protein Destination;
YPR185W	APG13	339a	Protein Destination; Intracellular Transport;	YGR253C	PUP2	339b	Unclassified Proteins;
YPR185W	APG13	340a	Protein Destination; Intracellular Transport;	YGR120C		340b	Unclassified Proteins;
YBR170C	NPL4	341a	Protein Destination; Intracellular Transport;	YGR048W	UFD1	341b	Unclassified Proteins;
YPR185W	APG13	342a	Protein Destination; Intracellular Transport;	YNL086W		342b	Unclassified Proteins;
YNL093W	YPT53	343a	Protein Destination; Intracellular Transport;	YNL032W	SIW14	343b	Unclassified Proteins;
YPR173C	VPS4	344a	Protein Destination; Intracellular Transport; Cellular Biogenesis; Cellular Organization;	YLR025W	SNF7	344b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;

YPL259C	APM1	345a	Protein Destination; Intracellular Transport; Cellular Biogenesis; Cellular Organization;	YKL135C	APL2	345b	Protein Destination; Intracellular Transport; Cellular Organization;
YUL154C	VPS35	346a	Protein Destination; Intracellular Transport; Cellular Biogenesis; Cellular Organization;	YGL166W	CUP2	346b	Transcription; Ionic Homeostasis; Cellular Organization;
YDR142C	PEX7	347a	Protein Destination; Intracellular Transport; Cellular Organization;	YIL160C	POT1	347b	Metabolism; Energy; Cellular Organization;
YNR006W	VPS27	348a	Protein Destination; Intracellular Transport; Cellular Organization;	YHL002W		348b	Signal Transduction;
YDR142C	PEX7	349a	Protein Destination; Intracellular Transport; Cellular Organization;	YGR239C		349b	Unclassified Proteins;
YDR142C	PEX7	350a	Protein Destination; Intracellular Transport; Cellular Organization;	YHR160C		350b	Unclassified Proteins;
YDL212W	SHR3	351a	Protein Destination; Signal Transduction; Cellular Organization;	YDR508C	GNP1	351b	Metabolism; Transport Facilitation;
YDR115W		352a	Protein Synthesis;	YKL142W	MRP8	352b	Protein Synthesis; Cellular Organization;
YER102W	RPS8B	353a	Protein Synthesis; Cellular Organization;	YBR135W	CKS1	353b	Cell Growth; Cell Division And DNA Synthesis;
YOR276W	CAF20	354a	Protein Synthesis; Cellular Organization;	YOL139C	CDC33	354b	Cell Growth; Cell Division And DNA Synthesis; Protein Synthesis; Cellular Organization;
YKL142W	MRP8	355a	Protein Synthesis; Cellular Organization;	YMR165C	SMP2	355b	Energy; Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis;
YKR026C	GCN3	356a	Protein Synthesis; Cellular Organization;	YKR026C	GCN3	356b	Protein Synthesis; Cellular Organization;
YKL142W	MRP8	357a	Protein Synthesis; Cellular Organization;	YKL142W	MRP8	357b	Protein Synthesis; Cellular Organization;
YMR309C	NIP1	358a	Protein Synthesis; Cellular Organization;	YNL244C	SUI1	358b	Protein Synthesis; Cellular Organization;
YLR264W	RPS28B	359a	Protein Synthesis; Cellular Organization;	YOL149W	DCP1	359b	Transcription;
YLR291C	GCD7	360a	Protein Synthesis; Cellular Organization;	YPL070W		360b	Unclassified Proteins;
YMR309C	NIP1	361a	Protein Synthesis; Cellular Organization;	YNL047C		361b	Unclassified Proteins;
YMR309C	NIP1	362a	Protein Synthesis; Cellular Organization;	YOR284W		362b	Unclassified Proteins;
YGL189C	RPS26A	363a	Protein Synthesis; Cellular Organization;	YLR435W		363b	Unclassified Proteins;
YER131W	RPS26B	364a	Protein Synthesis; Cellular Organization;	YLR435W		364b	Unclassified Proteins;
YLR264W	RPS28B	365a	Protein Synthesis; Cellular Organization;	YBR094W		365b	Unclassified Proteins;
YER102W	RPS8B	366a	Protein Synthesis; Cellular Organization;	YFL017C		366b	Unclassified Proteins;

YDR429C	TIF35	367a	Organization; Protein Synthesis; Cellular	YFL017C	367b	Unclassified Proteins;
YCR020C- A	MAK31	368a	Organization; Retrotransposons And Plasmid Proteins;	YEL053C	368b	Energy;
YHR158C	KEL1	369a	Signal Transduction;	YOR047C	369b	Metabolism; Transcription;
YHR158C	KEL1	370a	Signal Transduction;	YJR122W	370b	Transcription; Cellular Organization;
YHR158C	KEL1	371a	Signal Transduction;	YMR181C	371b	Unclassified Proteins;
YCR027C		372a	Signal Transduction;	YOL083W	372b	Unclassified Proteins;
YHL002W		373a	Signal Transduction;	YNR005C	373b	Unclassified Proteins;
YKL166C	TPK3	374a	Signal Transduction; Cellular Organization;	YIL033C	374b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YDR017C	KCS1	375a	Transcription;	YDR099W	375b	Cell Growth, Cell Division And DNA Synthesis;
YOR025W	HST3	376a	Transcription;	YLR403W	376b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YIL105C		377a	Transcription;	YER179W	377b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YDR028C		378a	Transcription;	YDR110W	378b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YIL105C		379a	Transcription;	YKL130C	379b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YML015C	TAF40	380a	Transcription;	YDR174W	380b	Cellular Organization;
YGL150C	INO80	381a	Transcription;	YOR355W	381b	Classification Not Yet Clear-Cut;
YGL150C	INO80	382a	Transcription;	YDL002C	382b	Classification Not Yet Clear-Cut;
YER127W	LCP5	383a	Transcription;	YDR299W	383b	Intracellular Transport;
YPR107C	YTH1	384a	Transcription;	YBR205W	384b	Metabolism; Protein Destination;
YGL221C	NIF3	385a	Transcription;	YGL221C	385b	Transcription;
YML015C	TAF40	386a	Transcription;	YDR167W	386b	Transcription; Cellular Organization;
YPR107C	YTH1	387a	Transcription;	YJR093C	387b	Transcription; Cellular Organization;
YDR439W	LRS4	388a	Transcription;	YCR086W	388b	Unclassified Proteins;
YCR004C	YCP4	389a	Transcription;	YDR032C	389b	Unclassified Proteins;
YER116C		390a	Transcription;	YGR024C	390b	Unclassified Proteins;
YIL105C		391a	Transcription;	YNL047C	391b	Unclassified Proteins;
YIR005W		392a	Transcription;	YGL174W	392b	Unclassified Proteins;
YDR311W	TFB1	393a	Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YGR120C	393b	Intracellular Transport; Cellular Organization;

YDR311W	TFB1	394a	Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YKL103C	LAP4	394b	Protein Destination; Cellular Organization;
YDR311W	TFB1	395a	Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YOL082W		395b	Unclassified Proteins;
YDR225W	HTA1	396a	Transcription; Cellular Organization;	YKR048C	NAP1	396b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Biogenesis; Cellular Organization;
YMR112C		397a	Transcription; Cellular Organization;	YBR253W	SRB6	397b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YGL208W	SIP2	398a	Transcription; Cellular Organization;	YGL115W	SNF4	398b	Metabolism; Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YGL122C	NAB2	399a	Transcription; Cellular Organization;	YKR026C	GCN3	399b	Protein Synthesis; Cellular Organization;
YDL160C	DHH1	400a	Transcription; Cellular Organization;	YOL149W	DCP1	400b	Transcription;
YGR158C	MTR3	401a	Transcription; Cellular Organization;	YDL111C	RRP42	401b	Transcription;
YKL028W	TFA1	402a	Transcription; Cellular Organization;	YDR311W	TFB1	402b	Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YGL237C	HAP2	403a	Transcription; Cellular Organization;	YBL021C	HAP3	403b	Transcription; Cellular Organization;
YGL237C	HAP2	404a	Transcription; Cellular Organization;	YOR358W	HAP5	404b	Transcription; Cellular Organization;
YBL021C	HAP3	405a	Transcription; Cellular Organization;	YOR358W	HAP5	405b	Transcription; Cellular Organization;
YOL123W	HRP1	406a	Transcription; Cellular Organization;	YGL122C	NAB2	406b	Transcription; Cellular Organization;
YOL135C	MED7	407a	Transcription; Cellular Organization;	YOR174W	MED4	407b	Transcription; Cellular Organization;
YPR110C	RPC40	408a	Transcription; Cellular Organization;	YNL113W	RPC19	408b	Transcription; Cellular Organization;
YJL025W	RRN7	409a	Transcription; Cellular Organization;	YBL014C	RRN6	409b	Transcription; Cellular Organization;
YMR270C	RRN9	410a	Transcription; Cellular Organization;	YBL025W	RRN10	410b	Transcription; Cellular Organization;
YOR159C	SME1	411a	Transcription; Cellular Organization;	YPR182W	SMX3	411b	Transcription; Cellular Organization;
YPR182W	SMX3	412a	Transcription; Cellular Organization;	YLR275W	SMD2	412b	Transcription; Cellular Organization;
YGR104C	SRB5	413a	Transcription; Cellular Organization;	YBR193C	MED8	413b	Transcription; Cellular Organization;

YDR308C	SRB7	414a	Transcription; Cellular Organization;	YOR174W	MED4	414b	Transcription; Cellular Organization;
YDR308C	SRB7	415a	Transcription; Cellular Organization;	YOL135C	MED7	415b	Transcription; Cellular Organization;
YGL112C	TAF60	416a	Transcription; Cellular Organization;	YMR236W	TAF17	416b	Transcription; Cellular Organization;
YKL028W	TFA1	417a	Transcription; Cellular Organization;	YKR062W	TFA2	417b	Transcription; Cellular Organization;
YOR210W	RPB10	418a	Transcription; Cellular Organization;	YGL166W	CUP2	418b	Transcription; Ionic Homeostasis; Cellular Organization;
YIR018W	YAP5	419a	Transcription; Cellular Organization;	YGL071W	RCS1	419b	Transcription; Ionic Homeostasis; Cellular Organization;
YDL160C	DHH1	420a	Transcription; Cellular Organization;	YEL015W		420b	Unclassified Proteins;
YPR110C	RPC40	421a	Transcription; Cellular Organization;	YLR238W		421b	Unclassified Proteins;
YDL150W	RPC53	422a	Transcription; Cellular Organization;	YKR025W		422b	Unclassified Proteins;
YDR088C	SLU7	423a	Transcription; Cellular Organization;	YDL144C		423b	Unclassified Proteins;
YMR039C	SUB1	424a	Transcription; Cellular Organization;	YMR316C-B		424b	Unclassified Proteins;
YGL112C	TAF60	425a	Transcription; Cellular Organization;	YMR255W		425b	Unclassified Proteins;
YDR002W		426a	Transcription; Intracellular Transport; Cellular Organization;	YKR048C	NAP1	426b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Biogenesis; Cellular Organization; Unclassified Proteins;
YLR293C	GSP1	427a	Transcription; Intracellular Transport; Cellular Organization;	YJR074W	MOG1	427b	Unclassified Proteins;
YOR185C	GSP2	428a	Transcription; Intracellular Transport; Cellular Organization;	YJR074W	MOG1	428b	Unclassified Proteins;
YLR216C	CPR6	429a	Transcription; Protein Destination; Cellular Organization;	YIR037W	HYR1	429b	Cell Rescue, Defense, Cell Death And Aging; Metabolism; Cell Growth, Cell Division And DNA Synthesis;
YBR237W	PRP5	430a	Transcription; Protein Destination; Cellular Organization;	YDR073W	SNF11	430b	Transcription; Cellular Organization;
YGR252W	GCN5	431a	Transcription; Protein Destination; Cellular Organization;	YDR448W	ADA2	431b	Transcription; Cellular Organization;
YBR052C		432a	Transport Facilitation;	YDR032C		432b	Transcription; Cellular Organization;
YKR104W		433a	Transport Facilitation; Cell Rescue, Defense, Cell Death And Aging;	YOL143C	RIB4	433b	Unclassified Proteins; Metabolism;
YLL028W		434a	Transport Facilitation; Cell Rescue, Defense, Cell Death And Aging;	YGL166W	CUP2	434b	Transcription; Ionic Homeostasis; Cellular Organization;
YIL013C	PDR11	435a	Transport Facilitation; Cellular	YDR174W		435b	Cellular Organization;

YOL130W	ALR1	436a	Organization; Transport Facilitation; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Ionic Homeostasis; Cellular Organization;	YGL025C	PGD1	436b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YOL130W	ALR1	437a	Transport Facilitation; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Ionic Homeostasis; Cellular Organization;	YLR291C	GCD7	437b	Protein Synthesis; Cellular Organization;
YMR243C	ZRC1	438a	Transport Facilitation; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Ionic Homeostasis; Cellular Organization;	YKL142W	MRP8	438b	Protein Synthesis; Cellular Organization;
YOL130W	ALR1	439a	Transport Facilitation; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Ionic Homeostasis; Cellular Organization;	YGL024W		439b	Unclassified Proteins;
YOL130W	ALR1	440a	Transport Facilitation; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Ionic Homeostasis; Cellular Organization;	YNL086W		440b	Unclassified Proteins;
YFL060C	SNO3	441a	Organization; Unclassified Proteins;	YMR096W	SNZ1	441b	Cell Growth, Cell Division And DNA Synthesis;
YDL012C		442a	Unclassified Proteins;	YDR151C	CTH1	442b	Cell Growth, Cell Division And DNA Synthesis;
YIL065C		443a	Unclassified Proteins;	YJR091C	JSN1	443b	Cell Growth, Cell Division And DNA Synthesis;
YLR392C		444a	Unclassified Proteins;	YJR091C	JSN1	444b	Cell Growth, Cell Division And DNA Synthesis;
YDR214W		445a	Unclassified Proteins;	YJL030W	MAD2	445b	Cell Growth, Cell Division And DNA Synthesis;
YNL127W		446a	Unclassified Proteins;	YKR055W	RHO4	446b	Cell Growth, Cell Division And DNA Synthesis;
YGR278W		447a	Unclassified Proteins;	YGR049W	SCM4	447b	Cell Growth, Cell Division And DNA Synthesis;
YMR322C		448a	Unclassified Proteins;	YMR096W	SNZ1	448b	Cell Growth, Cell Division And DNA Synthesis;
YBR190W		449a	Unclassified Proteins;	YLR117C	SYF3	449b	Cell Growth, Cell Division And DNA Synthesis;
YDL012C		450a	Unclassified Proteins;	YJL065C		450b	Cell Growth, Cell Division And DNA Synthesis;
YNR029C		451a	Unclassified Proteins;	YJL065C		451b	Cell Growth, Cell Division And DNA Synthesis;

YGL061C	DUO1	452a	Unclassified Proteins;	YER016W	BIM1	452b	Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Cellular Organization;
YOR353C		453a	Unclassified Proteins;	YHR102W	NRK1	453b	Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis;
YBR141C		454a	Unclassified Proteins;	YGL091C	NBP35	454b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YGR154C		455a	Unclassified Proteins;	YCR057C	PWP2	455b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YGR017W		456a	Unclassified Proteins;	YLR403W	SFP1	456b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YJL048C		457a	Unclassified Proteins;	YKL130C	SHE2	457b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YPR020W		458a	Unclassified Proteins;	YKL130C	SHE2	458b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YDL239C		459a	Unclassified Proteins;	YHR184W	SSP1	459b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YNL078W		460a	Unclassified Proteins;	YKR048C	NAP1	460b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Biogenesis; Cellular Organization;
YDR315C		461a	Unclassified Proteins;	YJR117W	STE24	461b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Biogenesis; Cellular Organization;
YLR200W	YKE2	462a	Unclassified Proteins;	YMR052W	FAR3	462b	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;
YDR200C		463a	Unclassified Proteins;	YMR052W	FAR3	463b	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;
YDR032C		464a	Unclassified Proteins;	YCL032W	STE50	464b	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;
YNL127W		465a	Unclassified Proteins;	YAL016W	TPD3	465b	Cell Growth, Cell Division And DNA Synthesis; Transcription;
YIL065C		466a	Unclassified Proteins;	YLR321C	SFH1	466b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Biogenesis; Cellular Organization;

YIL132C	467a	Unclassified Proteins;	YLR321C	SFH1	467b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Biogenesis; Cellular Organization;
YGL230C	468a	Unclassified Proteins;	YKL110C	KTH12	468b	Cell Rescue, Defense, Cell Death And Aging;
YBL101W-A	469a	Unclassified Proteins;	YBL043W	ECM13	469b	Cellular Biogenesis;
YGR068C	470a	Unclassified Proteins;	YBL102W	SFT2	470b	Cellular Organization;
YKL090W	471a	Unclassified Proteins;	YPL128C	TBF1	471b	Cellular Organization;
YPL260W	472a	Unclassified Proteins;	YIL144W	TID3	472b	Cellular Organization;
YKL002W	473a	Unclassified Proteins;	YMR117C		473b	Cellular Organization;
YBR141C	474a	Unclassified Proteins;	YDR372C		474b	Unclassified Proteins;
YMR095C	475a	Unclassified Proteins;	YNL333W	SNZ2	475b	Classification Not Yet Clear-Cut;
YFL060C	476a	Unclassified Proteins;	YNL333W	SNZ2	476b	Classification Not Yet Clear-Cut;
YDL012C	477a	Unclassified Proteins;	YOR355W	GDS1	477b	Classification Not Yet Clear-Cut;
YNL091W	478a	Unclassified Proteins;	YOR355W	GDS1	478b	Classification Not Yet Clear-Cut;
YMR312W	479a	Unclassified Proteins;	YHR187W	IKI1	479b	Classification Not Yet Clear-Cut;
YMR322C	480a	Unclassified Proteins;	YNL333W	SNZ2	480b	Classification Not Yet Clear-Cut;
YMR322C	481a	Unclassified Proteins;	YFL059W	SNZ3	481b	Classification Not Yet Clear-Cut;
YDR071C	482a	Unclassified Proteins;	YBR125C		482b	Classification Not Yet Clear-Cut;
YDR482C	483a	Unclassified Proteins;	YGL028C		483b	Classification Not Yet Clear-Cut;
YMR102C	484a	Unclassified Proteins;	YNL218W		484b	Classification Not Yet Clear-Cut;
YJL112W	485a	Unclassified Proteins;	YLL001W	DNM1	485b	Intracellular Transport; Cellular Biogenesis;
YDR472W	486a	Unclassified Proteins;	YKR068C	BET3	486b	Intracellular Transport; Cellular Organization;
YDR128W	487a	Unclassified Proteins;	YLR208W	SEC13	487b	Intracellular Transport; Cellular Organization;
YPR105C	488a	Unclassified Proteins;	YGL145W	TIP20	488b	Intracellular Transport; Cellular Organization;
YAL034W-A	489a	Unclassified Proteins;	YGR120C		489b	Intracellular Transport; Cellular Organization;
YDR472W	490a	Unclassified Proteins;	YBR254C		490b	Intracellular Transport; Cellular Organization;
YER157W	491a	Unclassified Proteins;	YGR120C		491b	Intracellular Transport; Cellular Organization;
YNR025C	492a	Unclassified Proteins;	YGR120C		492b	Intracellular Transport; Cellular Organization;
YOR353C	493a	Unclassified Proteins;	YGR120C		493b	Intracellular Transport; Cellular Organization;
YPR105C	494a	Unclassified Proteins;	YGR120C		494b	Intracellular Transport; Cellular Organization;
YFL010C	495a	Unclassified Proteins;	YDR515W	SLF1	495b	Ionic Homeostasis;
YEL041W	496a	Unclassified Proteins;	YJR049C	UTR1	496b	Ionic Homeostasis;
YGR163W	497a	Unclassified Proteins;	YML121W	GTR1	497b	Metabolism;
YNL311C	498a	Unclassified Proteins;	YKL001C	MET14	498b	Metabolism;

YOR138C	499a	Unclassified Proteins;	YEL062W	NPR2	499b	Metabolism;
YLL062C	500a	Unclassified Proteins;	YOL143C	RIB4	500b	Metabolism;
YBL101W.	501a	Unclassified Proteins;	YNL229C	URE2	501b	Metabolism;
A						
YDL012C	502a	Unclassified Proteins;	YFR047C		502b	Metabolism;
YDR132C	503a	Unclassified Proteins;	YJL218W		503b	Metabolism;
YGR294W	504a	Unclassified Proteins;	YHL018W		504b	Metabolism;
YIL008W	505a	Unclassified Proteins;	YHR111W		505b	Metabolism;
YNL311C	506a	Unclassified Proteins;	YIL074C		506b	Metabolism;
YFR042W	507a	Unclassified Proteins;	YPR159W	KRE6	507b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Cellular Organization;
						Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;
YML088W	508a	Unclassified Proteins;	YDR328C	SKP1	508b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;
						Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;
YGR122W	509a	Unclassified Proteins;	YLR025W	SNF7	509b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;
						Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;
YMR025W	510a	Unclassified Proteins;	YNR052C	POP2	510b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
						Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YML068W	511a	Unclassified Proteins;	YDR073W	SNF11	511b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
						Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YNL094W	512a	Unclassified Proteins;	YNL025C	SSN8	512b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
						Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YDR215C	513a	Unclassified Proteins;	YPL175W	SPT14	513b	Metabolism; Cellular Biogenesis; Cellular Organization;
						Metabolism; Energy; Metabolism; Energy; Metabolism; Energy; Metabolism; Energy; Cell Growth, Cell Division And DNA Synthesis; Protein Synthesis; Cellular Organization;
YAL032C	514a	Unclassified Proteins;	YLR345W		514b	Metabolism; Energy;
YLR465C	515a	Unclassified Proteins;	YML035C	AMD1	515b	Metabolism; Energy;
YDL012C	516a	Unclassified Proteins;	YIL172C		516b	Metabolism; Energy;
YAR014C	517a	Unclassified Proteins;	YER133W	GLC7	517b	Metabolism; Energy; Cell Growth, Cell Division And DNA Synthesis; Protein Synthesis; Cellular Organization;
						Metabolism; Energy; Cellular Organization;
YML053C	518a	Unclassified Proteins;	YJR009C	TDH2	518b	Metabolism; Energy; Cellular Organization;
YGR058W	519a	Unclassified Proteins;	YLR113W	HOG1	519b	Metabolism; Signal Transduction; Cell Rescue, Defense, Cell Death And Aging;

YCL046W	520a	Unclassified Proteins;	YGL115W	SNF4	520b	Metabolism; Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization; Metabolism; Transcription;
YPL039W	MET31	Unclassified Proteins;	YEL009C	GCN4	521b	Cellular Organization;
YGL242C	522a	Unclassified Proteins;	YKR099W	BAS1	522b	Metabolism; Transcription;
YDL076C	523a	Unclassified Proteins;	YLR098C	CHA4	523b	Cellular Organization;
YDL239C	524a	Unclassified Proteins;	YLR098C	CHA4	524b	Metabolism; Transcription;
YHR145C	525a	Unclassified Proteins;	YEL009C	GCN4	525b	Cellular Organization;
YDL110C	526a	Unclassified Proteins;	YKL015W	PUT3	526b	Metabolism; Transcription;
YGL230C	527a	Unclassified Proteins;	YDL210W	UGA4	527b	Cellular Organization;
YPL222W	528a	Unclassified Proteins;	YGR048W	UFD1	528b	Metabolism; Transport Facilitation; Intracellular Transport; Cellular Organization;
YIL151C	529a	Unclassified Proteins;	YLR121C	YPS4	529b	Protein Destination;
YLL049W	530a	Unclassified Proteins;	YNR069C		530b	Protein Destination;
YNR068C	531a	Unclassified Proteins;	YNR069C		531b	Protein Destination;
YAR031W	532a	Unclassified Proteins;	YBR217W		532b	Protein Destination; Cellular Biogenesis; Cellular Organization;
YAL034W-A	533a	Unclassified Proteins;	YKL103C	LAP4	533b	Protein Destination; Cellular Organization;
YPL019C	534a	Unclassified Proteins;	YHR060W	VMA22	534b	Protein Destination; Cellular Organization;
YPR105C	535a	Unclassified Proteins;	YHR060W	VMA22	535b	Protein Destination; Cellular Organization;
YOL105C	WSC3	Unclassified Proteins;	YGL153W	PEX14	536b	Protein Destination; Intracellular Transport; Cellular Organization;
YBR077C	537a	Unclassified Proteins;	YMR004W	MVP1	537b	Protein Destination; Intracellular Transport; Cellular Organization;
YPL151C	538a	Unclassified Proteins;	YOR036W	PEP12	538b	Protein Destination; Intracellular Transport; Cellular Organization;
YPR105C	539a	Unclassified Proteins;	YGL153W	PEX14	539b	Protein Destination; Intracellular Transport; Cellular Organization;
YDR482C	540a	Unclassified Proteins;	YOR276W	CAF20	540b	Protein Synthesis; Cellular Organization;
YBR270C	541a	Unclassified Proteins;	YKR026C	GCN3	541b	Protein Synthesis; Cellular Organization;
YER186C	542a	Unclassified Proteins;	YKR026C	GCN3	542b	Protein Synthesis; Cellular Organization;
YMR269W	543a	Unclassified Proteins;	YKR026C	GCN3	543b	Protein Synthesis; Cellular Organization;
YER082C	544a	Unclassified Proteins;	YKL142W	MRP8	544b	Protein Synthesis; Cellular Organization;

YMR210W	545a	Unclassified Proteins;	YKL142W	MRP8	545b	Organization; Protein Synthesis; Cellular
YDL063C	546a	Unclassified Proteins;	YPL131W	RPL5	546b	Organization; Protein Synthesis; Cellular
YLL027W	547a	Unclassified Proteins;	YGL189C	RPS26A	547b	Organization; Protein Synthesis; Cellular
YLL027W	548a	Unclassified Proteins;	YER131W	RPS26B	548b	Organization; Protein Synthesis; Cellular
YDR315C	549a	Unclassified Proteins;	YLR264W	RPS28B	549b	Organization; Protein Synthesis; Cellular
YCL020W	550a	Unclassified Proteins;	YFL002W-A		550b	Organization; Protein Synthesis; Cellular
YFL010C	551a	Unclassified Proteins;	YGR136W		551b	Organization; Protein Synthesis; Cellular
YGR058W	552a	Unclassified Proteins;	YGR136W		552b	Organization; Protein Synthesis; Cellular
YDR416W	553a	Unclassified Proteins;	YBR188C	NTC20	553b	Organization; Protein Synthesis; Cellular
YDR215C	554a	Unclassified Proteins;	YKR024C	DBP7	554b	Organization; Protein Synthesis; Cellular
YDR132C	555a	Unclassified Proteins;	YHR170W	NMD3	555b	Organization; Protein Synthesis; Cellular
YBR270C	556a	Unclassified Proteins;	YIL105C		556b	Organization; Protein Synthesis; Cellular
YDL146W	557a	Unclassified Proteins;	YKL070W		557b	Organization; Protein Synthesis; Cellular
YDR326C	558a	Unclassified Proteins;	YIL105C		558b	Organization; Protein Synthesis; Cellular
YGR250C	559a	Unclassified Proteins;	YIL001C		559b	Organization; Protein Synthesis; Cellular
YMR068W	560a	Unclassified Proteins;	YIL105C		560b	Organization; Protein Synthesis; Cellular
YPR082C	561a	Unclassified Proteins;	YBR055C	PRP6	561b	Organization; Protein Synthesis; Cellular
YDR313C	562a	Unclassified Proteins;	YPL133C	YPL133C	562b	Organization; Protein Synthesis; Cellular
YGR068C	563a	Unclassified Proteins;	YGL019W	CKB1	563b	Organization; Protein Synthesis; Cellular
YMR255W	564a	Unclassified Proteins;	YGL122C	NAB2	564b	Organization; Protein Synthesis; Cellular
YDL098C	565a	Unclassified Proteins;	YGR075C	PRP38	565b	Organization; Protein Synthesis; Cellular
YFL023W	566a	Unclassified Proteins;	YBR154C	RPB5	566b	Organization; Protein Synthesis; Cellular
YDR255C	567a	Unclassified Proteins;	YKL144C	RPC25	567b	Organization; Protein Synthesis; Cellular
YDR357C	568a	Unclassified Proteins;	YPR182W	SMX3	568b	Organization; Protein Synthesis; Cellular
YOL106W	569a	Unclassified Proteins;	YPR182W	SMX3	569b	Organization; Protein Synthesis; Cellular
YBR270C	570a	Unclassified Proteins;	YMR236W	TAF17	570b	Organization; Protein Synthesis; Cellular
YML114C	571a	Unclassified Proteins;	YDR167W	TAF25	571b	Organization; Protein Synthesis; Cellular
YDL063C	572a	Unclassified Proteins;	YDR381W	YRA1	572b	Organization; Protein Synthesis; Cellular

YNL171C	573a	Unclassified Proteins;	YCR106W	573b	Organization; Transcription; Cellular Organization;
YAL034W- A	574a	Unclassified Proteins;	YGL172W NUP49	574b	Transcription; Intracellular Transport; Cellular Organization;
YKR011C	575a	Unclassified Proteins;	YGL166W CUP2	575b	Transcription; Ionic Homeostasis; Cellular Organization;
YML006C	576a	Unclassified Proteins;	YGL166W CUP2	576b	Transcription; Ionic Homeostasis; Cellular Organization;
YOR220W	577a	Unclassified Proteins;	YGL166W CUP2	577b	Transcription; Ionic Homeostasis; Cellular Organization;
YHL006C	578a	Unclassified Proteins;	YNL021W HDA1	578b	Transcription; Protein Destination; Cellular Organization;
YDL012C	579a	Unclassified Proteins;	YHR032W	579b	Transport Facilitation; Cell Rescue, Defense, Cell Death And Aging;
YMR075C- A	580a	Unclassified Proteins;	YCR023C	580b	Transport Facilitation; Cell Rescue, Defense, Cell Death And Aging;
YGR113W	581a	Unclassified Proteins;	YGL061C DUO1	581b	Unclassified Proteins;
YGL061C	582a	Unclassified Proteins;	YDR016C	582a	Unclassified Proteins;
YAL036C	583a	Unclassified Proteins;	YDR152W	583b	Unclassified Proteins;
YAL032C	584a	Unclassified Proteins;	YPL151C	584b	Unclassified Proteins;
YDR490C	585a	Unclassified Proteins;	YHR207C	585b	Unclassified Proteins;
YDR490C	586a	Unclassified Proteins;	YIR044C	586b	Unclassified Proteins;
YDR490C	587a	Unclassified Proteins;	YLR466W	587b	Unclassified Proteins;
YLR082C	588a	Unclassified Proteins;	YLR082C	588b	Unclassified Proteins;
YDR416W	589a	Unclassified Proteins;	YJR050W	589b	Unclassified Proteins;
YDR016C	590a	Unclassified Proteins;	YGR129W	590b	Unclassified Proteins;
YHR016C	591a	Unclassified Proteins;	YLR243W	591b	Unclassified Proteins;
YHR016C	592a	Unclassified Proteins;	YMR255W	592b	Unclassified Proteins;
YHL006C	593a	Unclassified Proteins;	YDR078C	593b	Unclassified Proteins;
YNL056W	594a	Unclassified Proteins;	YNL032W	594b	Unclassified Proteins;
YFL023W	595a	Unclassified Proteins;	YLR200W	595b	Unclassified Proteins;
YAR031W	596a	Unclassified Proteins;	YCR030C	596b	Unclassified Proteins;
YBL101W- A	597a	Unclassified Proteins;	YFL002W-A	597b	Unclassified Proteins;
YBL101W- A	598a	Unclassified Proteins;	YJL162C	598b	Unclassified Proteins;
YBR103W	599a	Unclassified Proteins;	YIL112W	599b	Unclassified Proteins;
YBR228W	600a	Unclassified Proteins;	YLR135W	600b	Unclassified Proteins;
YDL012C	601a	Unclassified Proteins;	YHR140W	601b	Unclassified Proteins;
YDL071C	602a	Unclassified Proteins;	YDR183W	602b	Unclassified Proteins;
YDL071C	603a	Unclassified Proteins;	YEL068C	603b	Unclassified Proteins;
YDL071C	604a	Unclassified Proteins;	YFL017C	604b	Unclassified Proteins;
YDL071C	605a	Unclassified Proteins;	YGR269W	605b	Unclassified Proteins;
YDL071C	606a	Unclassified Proteins;	YNL155W	606b	Unclassified Proteins;

- 40 -

YJR136C	655a	Unclassified Proteins;	YKL033W	655b	Unclassified Proteins;
YKL090W	656a	Unclassified Proteins;	YGR024C	656b	Unclassified Proteins;
YKR007W	657a	Unclassified Proteins;	YBR077C	657b	Unclassified Proteins;
YKR022C	658a	Unclassified Proteins;	YBL010C	658b	Unclassified Proteins;
YKR060W	659a	Unclassified Proteins;	YDR179C	659b	Unclassified Proteins;
YKR083C	660a	Unclassified Proteins;	YKL052C	660b	Unclassified Proteins;
YLR015W	661a	Unclassified Proteins;	YDR469W	661b	Unclassified Proteins;
YLR065C	662a	Unclassified Proteins;	YDL149W	662b	Unclassified Proteins;
YLR315W	663a	Unclassified Proteins;	YDR383C	663b	Unclassified Proteins;
YLR328W	664a	Unclassified Proteins;	YGR010W	664b	Unclassified Proteins;
YLR328W	665a	Unclassified Proteins;	YLR328W	665b	Unclassified Proteins;
YLR424W	666a	Unclassified Proteins;	YKR022C	666b	Unclassified Proteins;
YML119W	667a	Unclassified Proteins;	YLL032C	667b	Unclassified Proteins;
YMR053W	668a	Unclassified Proteins;	YDR398W	668b	Unclassified Proteins;
YNL056W	669a	Unclassified Proteins;	YNL099C	669b	Unclassified Proteins;
YNL086W	670a	Unclassified Proteins;	YKL061W	670b	Unclassified Proteins;
YNL091W	671a	Unclassified Proteins;	YKL075C	671b	Unclassified Proteins;
YNL091W	672a	Unclassified Proteins;	YNL164C	672b	Unclassified Proteins;
YNL091W	673a	Unclassified Proteins;	YNL288W	673b	Unclassified Proteins;
YNL091W	674a	Unclassified Proteins;	YPL229W	674b	Unclassified Proteins;
YNL094W	675a	Unclassified Proteins;	YAL049C	675b	Unclassified Proteins;
YNL122C	676a	Unclassified Proteins;	YKL061W	676b	Unclassified Proteins;
YNR004W	677a	Unclassified Proteins;	YPL157W	677b	Unclassified Proteins;
YNR029C	678a	Unclassified Proteins;	YJL064W	678b	Unclassified Proteins;
YOL070C	679a	Unclassified Proteins;	YNL078W	679b	Unclassified Proteins;
YOR023C	680a	Unclassified Proteins;	YCR082W	680b	Unclassified Proteins;
YOR138C	681a	Unclassified Proteins;	YGR268C	681b	Unclassified Proteins;
YOR215C	682a	Unclassified Proteins;	YHR115C	682b	Unclassified Proteins;
YOR264W	683a	Unclassified Proteins;	YCR086W	683b	Unclassified Proteins;
YOR264W	684a	Unclassified Proteins;	YGR058W	684b	Unclassified Proteins;
YOR353C	685a	Unclassified Proteins;	YOL082W	685b	Unclassified Proteins;
YPL110C	686a	Unclassified Proteins;	YGR024C	686b	Unclassified Proteins;
YPL192C	687a	Unclassified Proteins;	YPL192C	687b	Unclassified Proteins;
YPR105C	688a	Unclassified Proteins;	YLR315W	688b	Unclassified Proteins;
YPR105C	689a	Unclassified Proteins;	YMR181C	689b	Unclassified Proteins;
YPR105C	690a	Unclassified Proteins;	YMR164C	690b	Unclassified Proteins;
YPR105C	691a	Unclassified Proteins;	YOR331C	691b	Unclassified Proteins;
YPR152C	692a	Unclassified Proteins;	YBR194W	692b	Unclassified Proteins;

In certain embodiments, the first polypeptide is labeled. In other embodiments, the second polypeptide is labeled, while in some embodiments, both the first and second polypeptides are labeled. Labeling can be performed using any art recognized method for labeling polypeptides. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

The invention also includes complexes of two or more polypeptides in which at least one of the polypeptides is present as a fragment of a complex-forming polypeptide according to the invention. For example, one or more polypeptides may include an amino acid sequence sufficient to bind to its corresponding polypeptide. A binding domain of a given first polypeptide can be any number of amino acids sufficient to specifically bind to, and complex with, the corresponding second polypeptide under conditions suitable for complex formation. The binding domain can be the minimal number of amino acids required to retain binding affinity, or may be a larger fragment or derivative of the polypeptides listed in Table 3, columns 1 and 4. Procedures for identifying binding domains can be readily identified by one of ordinary skill in the art and the procedures described herein. For example, nucleic acid sequences containing various portions of a "bait" protein can be tested in a yeast two hybrid screening assay in combination with a nucleic acid encoding the corresponding "prey" protein.

In certain embodiments, the "bait" polypeptides of the complex are polypeptides categorized, for example, as a "Metabolism" protein in the MIPS database. In some embodiments, the "prey" protein of the complex is also a "Metabolism" protein, while in other embodiments the "prey" protein is, for example, an "Unclassified" protein (*see* Table 3; *e.g.*, ProPair 195a-310a and ProPair 195b-310b). Other MIPS categories include, *e.g.*, "Cell Growth/Cell Division/DNA Synthesis" proteins (*see* Table 2).

In other embodiments, the complexes are human ortholog complexes, chimeric complexes, or specific complexes implicated in fungal pathways, as discussed in detail below.

Polypeptides forming the complexes according to the invention can be made using techniques known in the art. For example, one or more of the polypeptides in the complex can be chemically synthesized using art-recognized methods for polypeptide synthesis. These methods are common in the art, including synthesis using a peptide synthesizer. See, *e.g.*,
5 *Peptide Chemistry, A Practical Textbook*, Bodasnsky, Ed. Springer-Verlag, 1988; Merrifield, *Science* 232: 241-247 (1986); Barany, *et al*, *Intl. J. Peptide Protein Res.* 30: 705-739 (1987); Kent, *Ann. Rev. Biochem.* 57:957-989 (1988), and Kaiser, *et al*, *Science* 243: 187-198 (1989).

Alternatively, polypeptides can be made by expressing one or both polypeptides from a nucleic acid and allowing the complex to form from the expressed polypeptides. Any known
10 nucleic acids that express the polypeptides, whether yeast or human (or chimerics of these polypeptides) can be used, as can vectors and cells expressing these polypeptides. Sequences of yeast ORFs and human polypeptides as referenced in Tables 3 and 7 are publicly available, *e.g.* at the Saccharomyces Genome Database (SGD) and GenBank (*see, e.g.* Hudson *et al.*, *Genome Res.* 7: 1169-1173 (1997)). If desired, the complexes can then be recovered and
15 isolated.

Recombinant cells expressing the polypeptide, or a fragment or derivative thereof, may be obtained using methods known in the art, and individual gene product or complex may be isolated and analyzed (*See, e.g.*, *e.g.*, as described in Sambrook *et al.*, eds., *MOLECULAR CLONING: A LABORATORY MANUAL*, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold
20 Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., *CURRENT PROTOCOLS IN MOLECULAR BIOLOGY*, John Wiley & Sons, New York, NY, 1993). This is achieved by assays that are based upon the physical and/or functional properties of the protein or complex. The assays can include, *e.g.*, radioactive labeling of one or more of the polypeptide complex components, followed by analysis by gel electrophoresis, immunoassay, cross-linking to marker-labeled
25 products. Polypeptide complex may be isolated and purified by standard methods known in the art (either from natural sources or recombinant host cells expressing the proteins/protein complex). These methods can include, *e.g.*, column chromatography (*e.g.*, ion exchange, affinity, gel exclusion, reverse-phase, high pressure, fast protein liquid, etc), differential centrifugation, differential solubility, or similar methods used for the purification of proteins.

30 **Complexes Useful for Identifying Anti-Fungal Agents**

The invention further provides complexes of polypeptides useful, *inter alia*, in identifying agents that inhibit the growth of microorganisms such as fungi.

Human fungal infections have increased dramatically in incidence and severity in recent years. Advances in surgery and cancer treatments as well as the increasing use of broad-spectrum antimicrobials and the spread of HIV have increased the number of patients at risk for fungal infections. Most fungi are completely resistant to conventional antibacterial drugs.

The antifungal drugs presently available fall into several categories depending on their mode of action, as discussed below. Because several complexes according to the invention include proteins associated with these modes of action, the complexes can be used to identify anti-fungal agents.

Protein interactions which are useful for identifying anti-fungal agents are considered below.

(i) *Interference In Nuclear Division*

Griseofulvin interferes with nuclear division in fungal mitosis by disrupting the mitotic spindle and inhibiting cytoplasmic microtubule aggregation by interacting with polymerized microtubules. There is evidence that griseofulvin binds to a microtubule-associated protein in addition to binding to tubulin.

In accordance with the present invention, several interactions have presently been identified where one of the interacting partners is a microtubule or a microtubule-associated protein. Inhibiting any of these interactions could lead to the disruption of microtubules and interference in mitotic division, similar to the mode of action of griseofulvin, thereby providing a new means of inhibiting fungal activity. Accordingly, in some embodiments, the invention provides purified complexes of the proteins detailed in Table 4, below (interacting protein pairs are in bold, by row; a description of each protein follows).

Table 4: Microtubule-related interactions identified

APG7 Apg12p-activating enzyme, involved in autophagy cytoplasm-to-vacuole protein targeting, and peroxisome degradation pathways	AUT7 Forms a protein complex with Aut2p to mediate attachment of autophagosomes to microtubules. Aut7p has homology to LC3, a microtubule-associated protein from rat
DUO1 Protein that interacts with Dam1p and causes cell death upon overproduction, involved in mitotic spindle function	BIM1 Microtubule binding protein
BUB3 Protein required for cell cycle arrest in response to loss of microtubule function	MAD3 Checkpoint protein required for cell cycle arrest in response to loss of microtubule

	function
KAR4 Regulatory protein required for pheromone induction of karyogamy genes, defective in nuclear fusion because of defect in microtubule-dependent movement of nuclei	MUM2 Muddled Meiosis, mutant is sporulation defective and fails to perform premiotic DNA synthesis
CLN3 G1/S-specific cyclin that interacts with Cdc28p protein kinase to control events at START	MAD3 Checkpoint protein required for cell cycle arrest in response to loss of microtubule function
EBS1 Protein with similarity to Est1p (Telomere elongation protein)	MAD2 Spindle-assembly checkpoint protein
MSB2 Protein for which overproduction suppresses bud emergence defect of cdc24 mutant, putative integral membrane protein	MAD2 Spindle-assembly checkpoint protein
MSB2 Protein for which overproduction suppresses bud emergence defect of cdc24 mutant, putative integral membrane protein	MAD3 Checkpoint protein required for cell cycle arrest in response to loss of microtubule function
NUP157 Nuclear pore protein (nucleoporin)	MAD2 Spindle-assembly checkpoint protein
SAP4 Sit4p-associated protein (SIT4 is a protein phosphatase)	MAD2 Spindle-assembly checkpoint protein
SAP4 Sit4p-associated protein (SIT4 is a protein phosphatase)	MAD3 Checkpoint protein required for cell cycle arrest in response to loss of microtubule function
SIN4 Component of RNA polymerase II holoenzyme/mediator complex, involved in positive and negative regulation of transcription, possibly via changes in chromatin structure	MAD2 Spindle-assembly checkpoint protein
SIN4 Component of RNA polymerase II holoenzyme/mediator complex, involved in positive and negative regulation of transcription, possibly via changes in chromatin structure	MAD3 Checkpoint protein required for cell cycle arrest in response to loss of microtubule function
YDR214W Protein of unknown function	MAD2 Spindle-assembly checkpoint protein
YNL218W Protein with similarity to E. coli DNA polymerase III gamma and tau subunits	MAD2 Spindle-assembly checkpoint protein
MCM16 Protein involved in chromosome segregation, plays a nonessential role that governs the kinetochore-microtubule mediated process of chromosome Segregation	MCM22 Protein required for maintenance of chromosomes and minichromosomes
CYP2 Cyclophilin (peptidylprolyl isomerase), ER or	JSN1 Benomyl dependent tubulin mutant, Protein

secreted isoform, plays a role in the stress response	that when overexpressed can suppress the hyperstable microtubule phenotype of tub2-150
SPC34 Protein component of the spindle pole body	JSN1 Benomyl dependent tubulin mutant, Protein that when overexpressed can suppress the hyperstable microtubule phenotype of tub2-150
YIL065C Protein of unknown function	JSN1 Benomyl dependent tubulin mutant, Protein that when overexpressed can suppress the hyperstable microtubule phenotype of tub2-150
YLR392C Protein of unknown function	JSN1 Benomyl dependent tubulin mutant, Protein that when overexpressed can suppress the hyperstable microtubule phenotype of tub2-150

As described above, in certain embodiments of these complexes contain the binding domains, of the polypeptides recited in Table 4, while other embodiments contain conservative variants of these polypeptides, or polypeptides which contain the polypeptides recited in Table 4.

5 (ii) *Disruption of Ergosterol Biosynthesis*

Azoles are synthetic compounds that can be classified as imidazoles (ketoconazole, clotrimazole and miconazole) or triazoles (itraconazole and fluconazole). The antifungal activity of azole drugs result from their reduction in the biosynthesis of ergosterol, the main sterol in the cell membranes of fungi. Reduction of ergosterol alters the structure of the cytoplasmic membrane as well as the function of several membrane-bound enzymes (such as those involved in nutrient transport and chitin synthesis). The azole drugs reduce ergosterol synthesis by inhibiting the fungal cytochrome p450 enzymes, specifically they inhibit the sterol 14-alpha-demethylase, a microsomal cytochrome P450-dependent enzyme system, leading to a decrease in ergosterol and an accumulation of 14-alpha-methylsterols. There is some evidence that the primary target of the azoles is the heme protein, which cocatalyzes cytochrome P-450-dependent 14-alpha-dependent 14-alpha-demethylation of lanosterol. One interaction containing a heme biosynthesis protein has been presently been identified (Table 5). Disruption of this interaction could also lead to depletion of ergosterol and accumulation of sterol precursors, including 14-alpha-methylated sterols, forming a membrane with altered structure and function. Accordingly, in some embodiments, the invention provides a purified complex of the proteins recited in Table 5, below.

Table 5: Heme biosynthesis protein interaction identified

SED1 Abundant cell surface glycoprotein that may contribute to cell wall integrity and stress resistance	HEM13 Coproporphyrinogen III oxidase, oxygen-repressed, sixth step in heme biosynthetic pathway
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Complexes containing one or more variants of these polypeptides are within the scope of the present invention, as are polypeptides having amino acid sequences which include the polypeptides recited in Table 5.

(iii) *Cell Wall Synthesis Inhibition*

Fungi share many biochemical targets with other eukaryotic cells. However, the fungal cell wall is a unique organelle and contains compounds, such as mannan, chitin and glucans, that are unique to fungi. The cell wall is dynamic and essential to the viability of the fungi due to its roles in osmotic protection, transport of macromolecules, growth, conjugation and spore formation. Major disruption of the composition or organization of the cell wall deleteriously affects cell growth. A number of compounds have been discovered that inhibit the development of fungal cell walls. Two class of these antifungal drugs are echinocandins, which inhibit glucan synthesis, and nikkomycins, which inhibit chitin synthesis.

Several interactions between proteins localized to the cell wall or enzymes responsible for production of cell wall components have presently been identified. Inhibiting any of these interactions could lead to a disruption of the cell wall, hence providing new means for inhibiting fungal viability. Accordingly, in certain embodiments, the present invention provides purified complexes of the proteins detailed in Table 6, below.

Table 6: Cell wall-related protein interactions identified

CDC11 Septin, component of 10 nm filaments of mother-bud neck; involved in cytokinesis	SPR28 Septin-related protein expressed during sporulation
YFR042W Protein of unknown function	KRE6 Glucan synthase subunit required for synthesis of beta-1,6-glucan, involved in cell wall beta-glucan assembly
YDR482C Protein of unknown function	SCW11 Soluble cell wall protein
SMI1 Protein involved in (1,3)-beta-glucan synthesis, possibly through regulation of cell wall glucan and chitin synthesis; Chromatin binding protein	BAS1 Transcription factor regulating basal and induced activity of histidine and adenine biosynthesis genes

WSC3 Protein required for maintenance of cell wall integrity and for the stress response	PEX14 Peroxisomal peripheral membrane protein (peroxin) involved in import of peroxisomal matrix proteins
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Embodiments of these complexes containing the binding domains or conservative variants of these polypeptides are within the scope of the present invention, as are polypeptides which contain the polypeptides recited in Table 6.

5 **Complexes Containing One or More Human Polypeptides**

The invention also provides purified complexes of two or more human polypeptides. In some embodiments, the interacting polypeptides are human orthologs of the interacting yeast polypeptides. Human orthologs according to the invention are set out in Table 7, below.

10 Complexes of human ortholog binding domains, conservative variants, and polypeptides including the human orthologs recited in Table 7, are within the scope of the invention, as are labeled ortholog complexes and/or polypeptides.

Table 7: Human ortholog protein interactions

Yeast accno (bait)	Human ortholog accno	Human ortholog name	Human ortholog description	Yeast accno (prey)	Human ortholog accno	Human ortholog name	Human ortholog description
yai032c	Q13573	SKIP	Nuclear protein Skip	yrl345w	p16118	PFKFB1	6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase/6PF-2-K/FRU-2,6-P2ase liver isozyme
yai032c	Q13573	SKIP	Nuclear protein Skip	yrl423c	q02224	CENPE	Centromeric protein E/CENP-E protein
yai032c	Q13573	SKIP	Nuclear protein Skip	ypl151c	p35606	COPP	Beta subunit of coatomer complex
yai034w-a	P06468	TPM2	Fibroblast muscle-type tropomyosin	ygl172w	p49790	NUP153	Nuclear pore complex protein NUP153
yai034w-a	P07951	TPM2	Skeletal beta-tropomyosin	ygl172w	p35658	NUP214	Nuclear pore complex protein NUP214/CAN protein
yai034w-a	P35749	MYH11	Myosin heavy chain, smooth muscle isoform/SMMHC [FRAGMENT]	ygl172w	p52948	NUP98	Nuclear pore complex protein NUP98/Nudeoporin NUP98
yai034w-a	P49454	CENPF	CENP-F kinetochore protein	ygl172w	p23490	LOR	Loricrin
yai034w-a	Q15545	TAF2F	Transcription initiation factor TFIID 55 kD subunit	ygl172w	p09651	HNRPA1	Heterogenous nuclear ribonucleoprotein A1/helix-destabilizing protein/single-strand binding protein/HNRNP core protein A1
yai034w-a	P06468	TPM2	Fibroblast muscle-type tropomyosin	ygr120c	p49454	CENPF	CENP-F kinetochore protein
yai034w-a	P07951	TPM2	Skeletal beta-tropomyosin	ygr120c	p30622	RSN	Resilin
yai034w-a	P49454	CENPF	CENP-F kinetochore protein	ygr120c	p04114	APOB	Apolipoprotein B
yai033w	P78406	MRNP41	mRNA-associated protein mRNP 41	ybr175w	q14727	APAF1	Apoptotic protease activating factor 1/APAF-1
yai033w	Q05048	CSTF1	Cleavage stimulation factor, 50 kDa subunit	ybr175w	p35606	COPP	Beta subunit of coatomer complex
yai033w	Q09028	RBAP48	Chromatin assembly factor 1 P48 subunit/retinoblastoma binding protein P48	ybr175w	q15542	TAF2D	Transcription initiation factor TFIID 100 Kd subunit/TAFII-100/TAFII100
yai033w	Q15542	TAF2D	Transcription initiation factor TFIID 100 Kd subunit/TAFII-100/TAFII100	ybr175w	p04901	GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 1
yai033w	Q16576	RBBP7	Histone acetyl transferase type B subunit 2/retinoblastoma-binding protein	ybr175w	p43034	PAFAH1B1	Platelet-activating factor acetylhydrolase IB alpha subunit
yai014c	P19338	NCL	Nucleolin/protein C23	yer133w	p37140	PPP1CB	Serine/threonine-protein phosphatase PP1-beta catalytic subunit
yai014c	P23327	HRC	Sarcoplasmic reticulum histidine-rich calcium binding protein	yer133w	p08129	PPP1CA	Serine/threonine protein phosphatase PP1-alpha 1 catalytic subunit
yai014c	P35663	CYL1	Cyclin I	yer133w	p05323	PPP2CA	Serine/threonine protein phosphatase PP2A-alpha, catalytic subunit
yai014c	P46100	ATRX	Transcriptional regulator ATRX/X-linked helicase I/XX-linked nuclear protein	yer133w	p11082	PPP2CB	Serine/threonine protein phosphatase PP2A-beta, catalytic subunit
ybi101w-a	O15016	KIAA0298	Hypothetical protein KIAA0298	ybi043w	q06481	APLP2	Amyloid-like protein 2/APPH/amyloid protein homolog
ybi101w-a	O15016	KIAA0298	Hypothetical protein KIAA0298	yf002w-a	q01484	ANK2	Ankyrin, brain variant 1/ankyrin B
ybi101w-a	O15016	KIAA0298	Hypothetical protein KIAA0298	yj1162c	p31689	HSJ2	DNAJ protein homolog 2/HSJ-2
ybi105c	P05127	PRKCB	Protein kinase C-beta-2/PKC-beta-2	ymi109w	p46821	MAP1B	Microtubule-associated protein 1B
ybi105c	P17252	PRKCA	Protein kinase C alpha	ymi109w	q14669	TRIP12	Thyroid receptor interacting protein 12/KIAA0045
ybr006w	P30837	ALDH5	Mitochondrial aldehyde dehydrogenase X	ydr382w	p05387	RPLP2	60S acidic ribosomal protein P2

ybr006w	P00352	ALDH1	Aldehyde dehydrogenase, cytosolic/ALDH class 1/ALDH1/ALDH-E1	yki023w	p35579	MYH9	Myosin heavy chain, nonmuscle type A/cellular myosin heavy chain, type A/NMMHC-A
ybr006w	P05091	ALDH2	Aldehyde dehydrogenase, mitochondrial/class 2/ALDH2/ALDH-E2	yki023w	q08170	SFRS4	Pre-mRNA splicing factor SRp75
ybr006w	P30837	ALDH5	Mitochondrial aldehyde dehydrogenase X	yki023w	p35663	CYLC1	Cyclin I
ybr006w	P47895	ALDH6	Aldehyde dehydrogenase 6	yki023w	q14093	CYLC2	Cyclin II
ybr006w	P49189	ALDH9	Aldehyde dehydrogenase, E3 isozyme/gamma-aminobutyraldehyde dehydrogenase	yki023w	q14203	DCTN1	Dynactin, 150 kD isoform [fragment]
ybr006w	P51649	SSADH	Succinate semialdehyde dehydrogenase/NAD+-dependent succinate-semialdehyde dehydrogenase	yki023w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
ybr103w	O14727	APAF1	Apoptotic protease activating factor 1/APAF-1	yli112w	p55273	CDKN2D	Cyclin-dependent kinase 4 inhibitor D/P19INK4D
ybr103w	P43034	PAFAH1B1	Platelet-activating factor acetylhydrolase IB alpha subunit	yli112w	q01484	ANK2	Ankyrin, brain variant 1/ankyrin B
ybr103w	Q15269	PWP2H	Periodic tryptophan protein 2 homolog	yli112w	q01485	ANK2	Brain ankyrin variant 2
ybr103w	Q15542	TAF2D	Transcription initiation factor TFIID 100 Kd subunit/TAFII-100/TAFII100	yli112w	p20749	BCL3	B-cell lymphoma 3-encoded protein
ybr221c	P11177	PDHB	Pyruvate dehydrogenase E1-beta subunit	yir345w	q16875	F26P	6PF-2-K/FRU-2, 6-P2ase brain/placenta-type isozyme/6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase
ybr221c	P21953	BCKDHB	2-oxoisovalerate dehydrogenase beta subunit	yir345w	p16118	PFKFB1	6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase/6PF-2-K/FRU-2, 6-P2ase liver isozyme
ybr221c	P51854	TKT2	Transketolase 2	yir345w	q16877	F263	6PF-2-K/FRU-2, 6-P2ase testis-type isozyme/6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase
ybr244w	P07203	GPX1	Glutathione peroxidase	yir117c	q14690	KIAA0185	RBP5 protein homolog/KIAA0185 [fragment]
ybr244w	P18283	GPX2	Glutathione peroxidase-GI.	yir117c	q15431	SYCP1	Synaptonemal complex protein 1/SCP-1 protein
ybr270c	P30414	NKTR	NK-tumor recognition protein/Natural-killer cells cyclophilin-related protein	yir105c	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID
ybr270c	P30414	NKTR	NK-tumor recognition protein/Natural-killer cells cyclophilin-related protein	ykr026c	q14232	ELF2B1	Translation initiation factor eIF-2B alpha subunit
ybr270c	P30414	NKTR	NK-tumor recognition protein/Natural-killer cells cyclophilin-related protein	yir423c	q02224	CENPE	Centromeric protein E/CENP-E protein
ybr270c	P30414	NKTR	NK-tumor recognition protein/Natural-killer cells cyclophilin-related protein	Ymr236w	q16594	TAF2G	Transcription initiation factor TFIID 31 kD subunit
ybr274w	P53355	DAPK1	Death-associated protein kinase 1/DAP-kinase 1	yir258w	p54840	GYS2	Glycogen synthase, liver
ybr274w	P54646	PRKAA2	5'-AMP-activated protein kinase, catalytic alpha-2 chain	yir258w	p13807	GYS1	Muscle glycogen synthase
ybr274w	P27448	P78	Putative serine/threonine-protein kinase P78	Ymr255w	p46821	MAP1B	Microtubule-associated protein 1B
ybr274w	P51812	RPS6KA3	Ribosomal protein S6 kinase II alpha 3/insulin-stimulated protein kinase 1	Ymr255w	p29375	RBBP2	RBBP-2/reinoblastoma binding protein 2
ybr274w	P53355	DAPK1	Death-associated protein kinase 1/DAP-kinase 1	Ymr255w	q03111	ENL	ENL protein
ybr274w	P54646	PRKAA2	5'-AMP-activated protein kinase, catalytic alpha-2 chain	Ymr255w	p51825	MLLT2	AF-4 protein
ybr274w	q14012	CAMK1	Calcium/calmodulin-dependent protein kinase type I	Ymr255w	p11387	TOP1	Topoisomerase I
ybr274w	q15831	STK11	Serine/threonine-protein kinase 11	Ymr255w	p46939	UTRN	Utrrophin

ycd020w	o15016	KIAA0298	Hypothetical protein KIAA0298	yf002w-a	q01484	ANK2	Ankyrin, brain variant 1/ankyrin B
ycd024w	p15735	PHKG2	Phosphorylase kinase, testis/liver, gamma-2	ykr048c	q01105	SET	Set protein/HLA-DR associated protein I/PHAPII
ycd024w	p27448	P78	Putative serine/threonine-protein kinase P78	ykr048c	p46060	RANGAP1	RanGTPase activating protein 1
ycd024w	p53355	DAPK1	Death-associated protein kinase 1/DAP-kinase 1	ykr048c	q99457	NAP1L3	Nucleosome assembly protein 1-like.3
ycd024w	p54646	PRKAA2	5'-AMP-activated protein kinase, catalytic alpha-2 chain	ykr048c	p55209	NAP1L1	NAP-1/nucleosome assembly protein 1-like 1
ycd024w	q13131	PRKAA1	5'-AMP-activated protein kinase, catalytic alpha-1 chain	ykr048c	o15355	PPM1C	Protein phosphatase 2C gamma isoform/PP2C-GAMMA
ycd024w	q14012	CAMK1	Calcium/calmodulin-dependent protein kinase type I	ykr048c	q01534	TSPY	Homo sapiens testicular protein (TSPY) mRNA, complete cds.
ycd024w	q15831	STK11	Serine/threonine-protein kinase 11	ykr048c	p19338	NCL	Nucleolin/protein C23
ycd024w	q16566	CAMK4	calcium/calmodulin-dependent protein kinase IV	ykr048c	q99733	NAP1L4	Nucleosome assembly protein 2/nucleosome assembly protein 1-like 4
ycd024w	q16816	PHKG1	Phosphorylase B kinase gamma catalytic chain, skeletal muscle isoform	ykr048c	p21817	RYR1	Ryanodine receptor 1
ycd059c	p46821	MAP1B	Microtubule-associated protein 1B	ygl201c	p49736	MCM2	DNA replication licensing factor MCM2/KIAA0030
ycd063w	q05682	CALD1	Caldesmon/CDM	yfr423c	q02224	CENPE	Centromeric protein E/CENP-E protein
ycr009c	p15924	DSP	Desmoplakin I and II	ybr108w	p04280	PRB1	Salivary proline-rich protein/dclone CP3, CP4, and CP5
ycr009c	p49418	AMPH	Amphiphysin	ybr108w	p54259	DRPLA	Atrophin-1/dentatorubral-pallidoluysian atrophy protein
ydl006w	o15355	PPM1C	Protein phosphatase 2C gamma isoform/PP2C-GAMMA	ydr162c	p46108	CRK	Proto-oncogene C-CRK
ydl006w	p35813	PPM1A	Protein phosphatase 2C alpha	ydr162c	p00519	ABL1	Proto-oncogene tyrosine-protein kinase ABL/c-abl
ydl006w	p49593	KIAA0015	Putative protein phosphatase 2C/PP2C/KIAA0015	ydr162c	p51451	BLK	Tyrosine-protein kinase BLK
ydl012c	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	ydr151c	o15541	ZNF183	zinc finger protein 183
ydl012c	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	ydr151c	p26651	ZFP36	Tristetraprolin/TTP/ZFP-36
ydl012c	q10571	MN1	Probable tumor suppressor protein MN1	ydr151c	p47974	BRF2	TIS11D protein/butyrate response factor 2/EGF-response factor 2
ydl012c	q93074	KIAA0192	Hypothetical protein KIAA0192	ydr151c	q07352	BRF1	Tis11B protein/butyrate response factor 1/EGF-response factor 1
ydl012c	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	yfr047c	q15274	NADC	Nicotinamide-nucleotide pyrophosphorylase [carboxylating]/quinolinate phosphoribosyl transferase
ydl012c	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	yor355w	q14689	TRIP12	Thyroid receptor interacting protein 12/KIAA0045
ydl012c	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	yor355w	p42568	MLLT3	AF-9 protein
ydl013w	q07283	THH	Trichohyalin	ydr510w	p55854	SMT3H1	Ubiquitin-like protein SMT3A
ydl013w	q07283	THH	Trichohyalin	yer116c	p38398	BRCA1	BREAST CANCER, TYPE 1
ydl017w	p24941	CDK2	Cell division protein kinase 2	ycr050c	p49368	CCT3	T-complex protein 1, gamma subunit
ydl017w	p19784	CSNK2A2	Casein kinase II alpha'	ydl160c	p38919	NUK-34	Nuk_34 mRNA for translation initiation factor.
ydl017w	p24941	CDK2	Cell division protein kinase 2	ydl160c	q13838	BAT1	Probably ATP-dependent RNA helicase P47
ydl017w	q00526	CDK3	Cell division protein kinase 3	ydl160c	p04765	EIF4A1	Eukaryotic initiation factor 4A1
ydl017w	q00534	CDK6	Cell division protein kinase 6/PLSTIRE for serine/threonine protein kinase.	ydl160c	q14240	EIF4A2	Eukaryotic initiation factor 4A1
ydl017w	q00536	PCTK1	Serine/threonine protein kinase PCTAIRE-1	ydl160c	p26196	DDX6	Probable ATP-dependent RNA helicase P54

yd1017w	p24941	CDK2	Cell division protein kinase 2	yj1088w	p00480	OTC	Ornithine carbamoyltransferase [precursor]/OTCase/ornithine transcarbamylase
yd1074c	p11055	MYH3	Embryonic myosin heavy chain.	yj1423c	q15431	SYCP1	Synaptonemal complex protein 1/SCP-1 protein
yd1074c	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform	yj1423c	p12270	TPR	Nucleoprotein TPR
yd1074c	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	yj1423c	p30622	RSN	Resilin
yd1074c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle	yj1423c	p05787	KRT8	Keratin, type II cytoskeletal 8/cytokeratin 8/K8/CK8
yd1074c	p15924	DSP	Desmoplakin I and II	yj1423c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
yd1074c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	yj1423c	p11047	LAMC1	Laminin gamma-1 chain [precursor]/laminin B2 chain
yd1074c	p49454	CENPF	CENP-F kinetochore protein	yj1423c	p15924	DSP	Desmoplakin I and II
yd1074c	q02224	CENPE	Centromeric protein E/CENP-E protein	yj1423c	p49454	CENPF	CENP-F kinetochore protein
yd1074c	q03001	BPAG1	Bullous 230 kDa pemphigoid antigen 1	yj1423c	q02224	CENPE	Centromeric protein E/CENP-E protein
yd1090c	p49356	FNTB	farnesyl-protein transferase beta-subunit	yj1019w	p49354	FNTA	Protein farnesyltransferase alpha-subunit
yd1090c	p53609	PGGT1B	Geranylgeranyltransferase type I beta-subunit	yj1019w	q92696	RABGGTA	RAB geranylgeranyl transferase alpha subunit
yd1097c	q13098	GPS1	G protein pathway suppressor 1	yj1009c	p05412	JUN	Transcription factor AP-1/c-jun proto oncogene
yd1113c	p15924	DSP	Desmoplakin I and II	yj1036w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
yd1113c	q02224	CENPE	Centromeric protein E/CENP-E protein	yj1036w	p49454	CENPF	CENP-F kinetochore protein
yd1113c	p15924	DSP	Desmoplakin I and II	yj1423c	p49454	CENPF	CENP-F kinetochore protein
yd1113c	q02224	CENPE	Centromeric protein E/CENP-E protein	yj1423c	q02224	CENPE	Centromeric protein E/CENP-E protein
yd1150w	p05423	BN51T	BN51 protein	ykr025w	p39687	PHAP1	HLA-DR associated protein I
yd1150w	p06748	NPM1	Nucleophosmin	ykr025w	o15355	PPM1C	Protein phosphatase 2C gamma isoform/PP2C-GAMMA
yd1150w	p35663	CYLC1	Cyclin I	ykr025w	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein
yd1150w	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	ykr025w	p21815	IBSP	Bone sialoprotein II [precursor]/BSP/Cell-binding sialoprotein
yd1150w	p55081	MFAP1	Microfibrillar protein 1	ykr025w	p19338	NCL	Nucleolin/protein C23
yd1150w	q14093	CYLC2	Cyclin II	ykr025w	p17480	UBTF	Nucleolar transcription factor 1/upstream binding factor 1/UBF-1
yd1154w	p20585	MSH3	DNA mismatch repair protein MSH3	ygl025c	q02817	MUC2	Intestinal mucin 2/mucin 2
yd1154w	p43246	MSH2	DNA mismatch repair protein MSH2	ygl025c	q02078	MEF2A	Myocyte-specific enhancer factor 2A
yd1154w	p20585	MSH3	DNA mismatch repair protein MSH3	yj1144w	p49454	CENPF	CENP-F kinetochore protein
yd1154w	p43246	MSH2	DNA mismatch repair protein MSH2	yj1144w	q02224	CENPE	Centromeric protein E/CENP-E protein
yd1154w	p52701	MSH6	DNA mismatch repair protein MSH6/G/T mismatch binding protein	yj1144w	p15924	DSP	Desmoplakin I and II
yd1154w	p43246	MSH2	DNA mismatch repair protein MSH2	Ymr224c	p49959	MRE11A	Double-strand break repair protein MRE11A/MRE11 homolog
yd1155w	p14635	CCNB1	G2/mitotic-specific cyclin B1	ybr135w	p10275	AR	Androgen receptor
yd1203c	q14154	KIAA0141	Hypothetical protein KIAA0141	ygr058w	p28676	GCA	Grancalcin
yd1203c	q14154	KIAA0141	Hypothetical protein KIAA0141	yor372c	p54259	DRPLA	Atrophin-1/dentatorubral-pallidoluysian atrophy protein
yd1239c	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform	yj1423c	q15431	SYCP1	Synaptonemal complex protein 1/SCP-1 protein
yd1239c	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	yj1423c	p12270	TPR	Nucleoprotein TPR

[illegible]

ydr142c	p25388	GNB2-RS1	Guanine nucleotide-binding protein beta subunit-like protein 12.3	yil160c	p55084	HADHB	Trifunctional enzyme beta subunit, mitochondrial [precursor]
ydr142c	q09028	RBAP48	Chromatin assembly factor 1 P48 subunit/relinoblastoma binding protein P48	yil160c	p24752	AMLAAD	ALPHA-METHYLACETOACETICACIDURIA
ydr142c	q13216	CKN1	Cockayne syndrome WD-repeat protein CSA	yil160c	p42765	THIM	3-ketoacyl-CoA thiolase mitochondrial/mitochondrial 3-oxoacyl-CoA thiolase
ydr142c	q13610	PWP1	Periodic tryptophan protein 1 homolog/keratinocyte protein IEF SSP 9502	yil160c	p22307	SCP2	Non-specific lipid-transfer protein/sterol carrier protein
ydr142c	q16576	RBBP7	Histone acetyl transferase type B subunit 2/relinoblastoma-binding protein	yil160c	p09110	ACAA	X-sterol carrier protein 2
ydr148c	p10515	DLAT	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex/PDC-E2	ydr510w	q93068	SMT3H3	3-ketoacyl-CoA thiolase, peroxisomal/3-oxoacyl-CoA peroxisomal thiolase.
ydr148c	p11182	DBT	Lipoamide acyl transferase component of branched-chain alpha-keto acid dehydrogenase complex	ydr510w	p55855	SMT3H2	Ubiquitin-like protein SMT3C
ydr148c	p17677	GAP43	Neuromodulin/axonal membrane protein GAP-43	ydr510w	p55854	SMT3H1	Ubiquitin-like protein SMT3B
ydr200c	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	Ymr052w	p30622	RSN	Ubiquitin-like protein SMT3A
ydr200c	p49454	CENPF	CENP-F kinetochore protein	Ymr052w	p35580	MYH10	Reslin
ydr200c	p49454	CENPF	CENP-F kinetochore protein	ynl127w	p20309	CHRM3	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
ydr201w	p12270	TPR	CENP-F kinetochore protein	yil144w	p49454	CENPF	Muscarinic acetylcholine receptor M3
ydr201w	p30622	RSN	Nucleoprotein TPR	yil144w	q02224	CENPE	CENP-F kinetochore protein
ydr218c	q43236	PNUTL2	Peanut-like protein 2/Brain protein H5	yj076c	q14141	KIAA0128	Centromeric protein E/CENP-E protein
ydr218c	q14141	KIAA0128	Septin 2 homolog [fragment]	yj076c	q15019	NEDD5	Septin 2 homolog [fragment]
ydr218c	q15019	NEDD5	NEDD5 protein homolog/KIAA0158	yj076c	q16643	DBN1	NEDD5 protein homolog/KIAA0158
ydr218c	q16181	CDC10	CDC10 protein homolog	yj076c	q16181	CDC10	Drebin E
ydr225w	p02261	H2AFA	Histone H2A.1	yj076c	p46060	RANGAP1	CDC10 protein homolog
ydr225w	p04908	none	Histone H2A.5	Ykr048c	q99457	NAP1L3	RanGTPase activating protein 1
ydr225w	p16104	H2AX	Histone H2A.X	Ykr048c	q99733	NAP1L4	Nucleosome assembly protein 1-like3
ydr225w	p28001	H2AFO	Histone H2A.2/H2A/O	Ykr048c	p55209	NAP1L1	Nucleosome assembly protein 2/nucleosome assembly protein 1-like 4
ydr228c	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	yfr423c	p49454	CENPF	NAP1-nucleosome assembly protein 1-like 1
ydr228c	p54252	MJD1	Machado-joseph disease protein 1	yfr423c	q02224	CENPE	CENP-F kinetochore protein
ydr228c	q10571	MN1	Probable tumor suppressor protein MN1	yfr423c	p13535	MYH8	Centromeric protein E/CENP-E protein
ydr228c	q93074	KIAA0192	Hypothetical protein KIAA0192	yfr423c	p15924	DSP	Myosin heavy chain, perinatal skeletal muscle
ydr259c	p11055	MYH3	Embryonic myosin heavy chain.	yfr423c	p15924	DSP	Desmoplakin I and II
ydr259c	p15924	DSP	Desmoplakin I and II	yfr423c	p49454	CENPF	Desmoplakin I and II
ydr259c	p49454	CENPF	CENP-F kinetochore protein	yfr423c	q02224	CENPE	CENP-F kinetochore protein
ydr308c	p24928	POLR2A	DNA-directed RNA polymerase II largest subunit.	yor174w	p49321	NASP	Centromeric protein E/CENP-E protein
ydr308c	q03001	BPAG1	Bullous 230 kDa pemphigoid antigen 1	yor174w	p35580	MYH10	Nuclear autoantigenic sperm protein
ydr311w	p32780	BTF2	Basic transcription factor 62kD subunit	yor174w	p04114	APOB	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
ydr311w	p32780	BTF2	Basic transcription factor 62kD subunit	yfr423c	q02224	CENPE	Apolipoprotein B
							Centromeric protein E/CENP-E protein

ydr328c	p07199	CENP-B	Major centromere autoantigen B/centromere protein B	yf009w	p35606	COPP	Beta subunit of coatomer complex
ydr328c	p17480	UBTF	Nucleolar transcription factor 1/upstream binding factor 1/UBF-1	yf009w	q15542	TAF2D	Transcription initiation factor TFIID 100 Kd subunit/TAFII-100/TAFII100
ydr328c	p19338	NCL	Nucleolin/protein C23	yf009w	p04901	GNB1	Guanine nucleotide-binding protein G(i)/G(s)/G(t) beta subunit 1
ydr328c	p34991	TCEB1L	Cyclin A/CDK2-associated p19	yf009w	p43034	PAFAH1B1	Platelet-activating factor acetylhydrolase IB alpha subunit
ydr376w	p22570	FDXR	NADPH:adrenodoxin oxidoreductase	ycr093w	p54252	MJD1	Machado-Joseph disease protein 1
ydr376w	p22570	FDXR	NADPH:adrenodoxin oxidoreductase [precursor]/adrenodoxin reductase/ferredoxin-NADP+ reductase	yir024c	p49321	NASP	Nuclear autoantigenic sperm protein
ydr388w	p14317	HCLS1	Hematopoietic lineage cell specific protein	ycr009c	p15924	DSP	Desmoplakin I and II
ydr388w	p49418	AMPH	Amphiphysin	ycr009c	p49418	AMPH	Amphiphysin
ydr394w	p17980	PSMC3	26S protease regulatory subunit 6A/TAT-binding protein 1/TBP-1	ygr232w	q06547	E4TF1B	GA binding protein beta-1 chain
ydr394w	p35998	PSMC2	26S protease regulatory subunit 7/MSS1 protein	ygr232w	q01485	ANK2	Brain ankyrin variant 2
ydr394w	p43686	PSMC4	26S protease regulatory subunit 6B/TAT-binding protein-7/TBP-7	ygr232w	p53355	DAPK1	Death-associated protein kinase 1/DAP-kinase 1
ydr394w	p47210	PSMC5	26S proteasome regulatory subunit 8/proteasome subunit p45	ygr232w	p20749	BCL3	B-cell lymphoma 3-encoded protein
ydr394w	q03527	PSMC1	26S protease (S4) regulatory subunit	ygr232w	q01484	ANK2	Ankyrin, brain variant 1/ankyrin B
ydr394w	q92524	PSMC6	26S protease regulatory subunit S10B/proteasome subunit P42	ygr232w	p42773	CDN2C	Cyclin dependent kinase 6 inhibitor
ydr408c	p22102	GART	Trifunctional purine biosynthetic protein adenosine-3	ycr063w	p41223	EDG2	G10 protein homolog
ydr408c	p22102	GART	Trifunctional purine biosynthetic protein adenosine-3	ygr174w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
ydr416w	q14690	KIAA0185	RRP5 protein homolog/KIAA0185 [fragment]	ygr129w	q02224	CENPE	Centromeric protein E/CENP-E protein
ydr429c	p33240	CSTF2	Cleavage stimulation factor, 64 kD subunit	yf0117c	p08578	SNRPE	Small nuclear ribonucleoprotein E/snRNP-E
ydr439w	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle	ycr086w	p39880	CUTL1	CCAAT displacement protein/CDP
ydr477w	p54646	PRKAA2	5'-AMP-activated protein kinase, catalytic alpha-2 chain	ygr027c	p10451	SPP1	Osteopontin [precursor]
ydr482c	p42566	EPS15	Epidermal growth factor receptor substrate 15	ygl028c	q02505	MUC3	Mucin 3 [fragments]/intestinal mucin 3
ydr482c	q02224	CENPE	Centromeric protein E/CENP-E protein	q02817	q02817	MUC2	Intestinal mucin 2/mucin 2
ydr490c	p17612	PRKACA	cAMP-dependent protein kinase catalytic subunit type alpha	q02505	q02505	MUC3	Mucin 3 [fragments]/intestinal mucin 3
ydr018c	p02546	LMN1	Lamin C	p50502	p50502	HIP	Progesterone receptor-associated p48 protein
ydr018c	p02545	LMN1	Lamin A/70 kD Lamin	p30622	p30622	RSN	Restin
ydr018c	p02546	LMN1	Lamin C	ygr117c	p49454	CENPF	CENP-F kinetochore protein
ydr018c	p35749	MYH11	Myosin heavy chain, smooth muscle isoform/SMMHC [FRAGMENT]	ygr117c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
ydr018c	q07283	THH	Trichohyalin	ygr117c	p11055	MYH3	Embryonic myosin heavy chain
ydr018c	q93074	KIAA0192	Hypothetical protein KIAA0192	ygr117c	p42566	EPS15	Epidermal growth factor receptor substrate 15
ydr023w	p32322	PYCR1	Pyroline 5-carboxylate reductase	ygr023w	p32322	PYCR1	Pyroline 5-carboxylate reductase

yer082c	p11016	GNB2	Guanine nucleotide-binding protein beta subunit 2	ykl142w	p07942	LAMB1	Laminin beta-1 chain/Laminin B1 chain
yer102w	p09058	RPS8	40S ribosomal protein S8	ybr135w	p10275	AR	Androgen receptor
yer102w	p09058	RPS8	40S ribosomal protein S8	yfl017c	p08578	SNRPE	Small nuclear ribonucleoprotein E/snRNP-E
yer106w	q13416	ORC2L	Origin recognition complex subunit 2	ydr086w	p39880	CUTL1	CCAAT displacement protein/CDP
yer127w	p30622	RSN	Restin	ydr299w	p19338	NCL	Nucleolin/protein C23
yer127w	p35663	CYLC1	Cyclin I	ydr299w	p46060	RANGAP1	RangGTPase activating protein 1
yer127w	p35749	MYH11	Myosin heavy chain, smooth muscle isoform/SMMHC [FRAGMENT]	ydr299w	p07197	NEFM	Neurofilament triplet M protein/160 Kd neurofilament protein/NF-M
yer127w	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase III-X-linked nuclear protein	ydr299w	p21817	RYR1	Ryanodine receptor 1
yer127w	q01484	ANK2	Ankyrin, brain variant 1/ankyrin B	ydr299w	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase III-X-linked nuclear protein
yer131w	q06722	RPS26	Ribosomal protein S26	ydr299w	p27797	CALR	Calreticulin/52kD ribonucleoprotein autoantigen RO/SS-A
yer133w	p05323	PPP2CA	Serine/threonine protein phosphatase PP2A-alpha, catalytic subunit	ynl233w	p35251	RFC1	Replication factor C large subunit/activator 1140 Kd subunit
yer133w	p08129	PPP1CA	Serine/threonine protein phosphatase PP1-alpha 1 catalytic subunit	ynl233w	p35663	CYLC1	Cyclin I
yer133w	p11082	PPP2CB	Serine/threonine protein phosphatase PP2A-beta, catalytic subunit	ynl233w	p51825	MLLT2	AF-4 protein
yer133w	p36873	PPP1CC	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	ynl233w	p46821	MAP1B	Microtubule-associated protein 1B
yer133w	p37140	PPP1CB	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	ynl233w	p35659	DEK	Dek protein
yer144c	o00507	FAF-Y	Probable ubiquitin carboxyl-terminal hydrolase FAF-Y	ybr059c	q16816	PHKG1	Phosphorylase B kinase gamma catalytic chain, skeletal muscle isoform
yer144c	p45974	USP5	Ubiquitin carboxyl-terminal hydrolase 5/isopeptidase T	ybr059c	p51956	NEK3	Serine/threonine-protein kinase NEK3 [fragment]
yer144c	p51784	USP11	Ubiquitin C-terminal hydrolase 11	ybr059c	p49137	MAPKAPK-2	Map kinase-activated protein kinase 2
yer144c	p54578	USP14	Queuine tRNA-ribosyl transferase/tRNA-guanine transglycosylase	ybr059c	p51955	NEK2	Serine/threonine-protein kinase NEK2
yer144c	q02817	MUC2	Intestinal mucin 2/mucin 2	ybr059c	p15735	PHKG2	Phosphorylase kinase, testis/liver, gamma-2
yer144c	q29955	USP13	Ubiquitin carboxyl-terminal hydrolase 13/isopeptidase T-3	ybr059c	q13177	PAK2	Serine/threonine-protein kinase PAK-gamma
yer144c	q93008	USP9X	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	ybr059c	p27448	P78	Putative serine/threonine-protein kinase P78
yer144c	q93009	USP7	Ubiquitin carboxyl-terminal hydrolase 7/herpesvirus associated ubiquitin-specific protease	ybr059c	p51957	STK2	Serine/threonine-protein kinase NRK2
yer179w	q06609	RAD51	DNA repair protein RAD51	yer179w	q06609	RAD51	DNA repair protein RAD51
yer179w	q14565	DMC1	Meiotic recombination protein DMC1/LIM15 homolog	yer179w	q14565	DMC1	Meiotic recombination protein DMC1/LIM15 homolog
yfl010c	p02812	PRB2	Salivary proline-rich protein/Clone CP7	ygr136w	p29354	GRB2	Growth factor receptor-bound protein 2
yfl010c	p04280	PRB1	Salivary proline-rich protein/done CP3, CP4, and CP5	ygr136w	p06241	FYN	Proto-oncogene tyrosine-protein kinase FYN/SYN
yfl010c	p10161	PRB4	Salivary proline-rich protein PO [fragment]/allele M	ygr136w	p14317	HCLS1	Hematopoietic lineage cell specific protein
yfl010c	p10162	PRB4	Salivary proline-rich protein PO [fragment]/allele K	ygr136w	p19878	NCF2	Neutrophil cytosol factor 2/NCF-2/ neutrophil NADPH oxidase factor 2/P67-PHOX
yfl010c	p17600	SYN1	Synapsin I/brain protein 4.1	ygr136w	q92794	MOZ	Monocytic leukemia zinc finger protein

yfl010c	p22670	RFX1	MHC class II regulatory factor RFX1	ygr136w	q15811	ITSN	Intersectin/SH3 domain-containing protein SH3P17
yfl010c	p23246	PSF	PTB-associated splicing factor	ygr136w	p16333	NCK	Cytoplasmic protein NCK
yfl010c	p35637	FUS	RNA-binding protein FUS/TLS	ygr136w	p46108	CRK	Proto-oncogene C-CRK
yfl010c	q22793	CREBBP	CREB-BINDING PROTEIN	ygr136w	p07947	YES1	Proto-oncogene tyrosine-protein kinase YES/C-YES
yfl010c	q22794	MOZ	Monocytic leukemia zinc finger protein	ygr136w	p15498	VAV	Vav proto-oncogene
yfl010c	q99217	AIH1	AMELOGENESIS IMPERFECTA 1, HYPOPLASTIC TYPE	ygr136w	p46109	CRKL	Crk-like protein
yfl010c	p02812	PRB2	Salivary proline-rich protein/Clone CP7	yor197w	p02812	PRB2	Salivary proline-rich protein/Clone CP7
yfl010c	p04280	PRB1	Salivary proline-rich protein/clone CP3, CP4, and CP5	yor197w	p04280	PRB1	Salivary proline-rich protein/clone CP3, CP4, and CP5
yfl010c	p10161	PRB4	Salivary proline-rich protein PO [fragment]/allele M	yor197w	p54253	SCA1	Alaxin-1/Spinocerebellar ataxia type 1 protein
yfl010c	p22670	RFX1	MHC class II regulatory factor RFX1	yor197w	q09472	EP300	E1A-associated protein P300
yfl010c	p23246	PSF	PTB-associated splicing factor	yor197w	q93074	KIAA0192	Hypothetical protein KIAA0192
yfl010c	p35637	FUS	RNA-binding protein FUS/TLS	yor197w	p42858	HD	Huntingtin/huntington's disease protein
yfl010c	q99217	AIH1	AMELOGENESIS IMPERFECTA 1, HYPOPLASTIC TYPE	yor197w	q01844	EWSR1	RNA-binding protein EWS
yfl023w	q02224	CENPE	Centromeric protein E/CENP-E protein	ybr154c	p19388	POLR2E	DNA-directed RNA polymerase II 23 kD polypeptide/RPB25/XAP4
yfl023w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMHC-B	yir200w	p49454	CENPF	CENP-F kinetochore protein
yfl023w	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase III-X-linked nuclear protein	yir200w	q08379	GOLGA2	Golgin-95
yfl023w	p48681	NES	Nestin	yir200w	p42566	EPS15	Epidermal growth factor receptor substrate 15
yfl023w	q02224	CENPE	Centromeric protein E/CENP-E protein	yir200w	q02224	CENPE	Centromeric protein E/CENP-E protein
yfl024c-a	p14317	HCLS1	Hematopoietic lineage cell specific protein	ybl007c	q99102	MUC4	Tracheo-bronchial mucin 4/mucin 4 [fragment]
yfl024c-a	p16333	NCK	Cytoplasmic protein NCK	ybl007c	p16333	NCK	Cytoplasmic protein NCK
yfl024c-a	p29354	GRB2	Growth factor receptor-bound protein 2	ybl007c	p29354	GRB2	Growth factor receptor-bound protein 2
yfl024c-a	p41240	CSK	Tyrosine-protein kinase CSK	ybl007c	p06241	FYN	Proto-oncogene tyrosine-protein kinase FYN/SYN
yfl024c-a	p46109	CRKL	Crk-like protein	ybl007c	p09769	M19722	Human fgr proto-oncogene encoded p55-c-fgr protein, complete cds.
yfl024c-a	p98171	RGCI	RHO-GAP hematopoietic protein C1	ybl007c	q15811	ITSN	Intersectin/SH3 domain-containing protein SH3P17
yfl024c-a	q13813	SPTA2	Spectrin alpha chain, brain/nonerythroid alpha-spectrin	ybl007c	p07947	YES1	Proto-oncogene tyrosine-protein kinase YES/C-YES
yfl024c-a	q15811	ITSN	Intersectin/SH3 domain-containing protein SH3P17	ybl007c	q14687	KIAA0182	Hypothetical protein KIAA0182
yfl024c-a	p46109	CRKL	Crk-like protein	ygr268c	q92794	MOZ	Monocytic leukemia zinc finger protein
yfl047c	q15274	NADC	Nicotinate-nucleotide pyrophosphorylase [carboxylating]/quinolate phosphoribosyl transferase	yfr047c	q15274	NADC	Nicotinate-nucleotide pyrophosphorylase [carboxylating]/quinolate phosphoribosyl transferase
ygl058w	p23567	UBE2B	Ubiquitin-conjugating enzyme E2-17 kD	ygr066w	q00755	PML	Probable transcription factor PML
ygl058w	p47986	UBE2D3	Ubiquitin-conjugating enzyme E2-17 kD 3	ygr066w	p35227	MEL18	DNA-binding protein MEL-18/Zinc finger protein 144
ygl058w	p49459	UBE2A	Ubiquitin-conjugating enzyme E2-17 kD/HRGA	ygr066w	p15918	RAG1	V(D)J recombination activating protein 1
ygl058w	p50550	UBE2I	Ubiquitin conjugating enzyme E2-18 kD	ygr066w	o15541	ZNF183	zinc finger protein 183
ygl058w	p51668	UBE2D1	Ubiquitin conjugating enzyme E2-17 kD	ygr066w	p35226	BM11	DNA-binding protein BM11
ygl058w	p51669	UBE2D2	Ubiquitin conjugating enzyme E2-17 kD 2	ygr066w	p38398	BRCA1	BREAST CANCER, TYPE 1
ygl058w	p51965	UBE2E1	Ubiquitin conjugating enzyme E2-21 kD UBCH6	ygr066w	p29591	PML	Probable transcription factor PML

ygl058w	p56554	UBE2G2	Ubiquitin-conjugating enzyme E2 G2	ycr066w	p29592	PML	Probable transcription factor PML
ygl058w	q16781	UBE2N	Ubiquitin-conjugating enzyme E2-17 kD	ycr066w	p29590	PML	Probable transcription factor PML
ygl058w	q99462	UBE2G1	Ubiquitin-conjugating enzyme E2 G1	ycr066w	p29593	PML	Probable transcription factor PML
ygl112c	p49848	TAF2E	Transcription initiation factor TFIID 70 kD	Ymr236w	q16594	TAF2G	Transcription initiation factor TFIID 31 kD subunit
ygl112c	p49848	TAF2E	subunit/TAFII-70	Ymr255w	p51825	MLLT2	AF-4 protein
ygl115w	p54619	PRKAG1	5'-AMP-activated protein kinase, gamma-1 subunit	Yer027c	p10451	SPP1	Osteopontin [precursor]
ygl122c	p42858	HD	Huntingtin/huntington's disease protein	Ykr026c	q14232	ELF2B1	Translation initiation factor eIF-2B alpha subunit
ygl122c	q14814	MEF2D	Myocyte-specific enhancer factor 2D	Ykr026c	p49770	EIF2B2	Translation initiation factor EIF-2B beta subunit/S20iil15
ygl150c	o14647	CHD2	Chromodomain-helicase-DNA-binding protein 2/CHD-2	Ydl002c	p17480	UBTF	Nucleolar transcription factor 1/upstream binding factor 1/UBF-1
ygl150c	p19338	NCL	Nucleolin/protein C23	Ydl002c	p36402	TCF7	T-cell-specific transcription factor 1/TCF-1
ygl150c	p28370	SMARCA1	Possible global transcription activator SNF2L1	Ydl002c	q00059	TCF6L1	Mitochondrial transcription factor 1
ygl150c	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	Ydl002c	p26583	HMG2	High mobility group protein HMG2/HMG-2
ygl150c	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	Ydl002c	q06945	SOX4	Transcription factor SOX-4
ygl150c	p51532	SMARCA4	Possible global transcription activator SNF2L4/BRG-1	Ydl002c	q08945	SSRP1	Structure-specific recognition protein 1
ygl150c	q03468	CSB	Excision repair protein ERCC-6/cockayne syndrome protein CSB	Ydl002c	p09429	HMG1	High mobility group-1 protein
ygl150c	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	Yor355w	q14669	TRIP12	Thyroid receptor interacting protein 12/KIAA0045
ygl155w	q03468	CSB	Excision repair protein ERCC-6/cockayne syndrome protein CSB	Yor355w	p42568	MLLT3	AF-9 protein
ygl155w	p49356	FNTB	farnesyl-protein transferase beta-subunit	Ykl019w	p49354	FNTA	Protein farnesyltransferase alpha-subunit
ygl155w	p53609	PGGT1B	Geranylgeranyltransferase type I beta-subunit	Ykl019w	q92696	RABGGTA	RAB geranylgeranyl transferase alpha subunit
ygl158w	p15735	PHKG2	Phosphorylase kinase, testis/liver, gamma-2	Ylr113w	p53779	MAPK10	Mitogen-activated protein kinase 10
ygl158w	p27448	P78	Pulative serine/threonine-protein kinase P78	Ylr113w	p53778	MAPK12	Mitogen-activated protein kinase 12/ERK6/extracellular signal-regulated kinase 6
ygl158w	p49137	MAPKAPK-2	Map kinase-activated protein kinase 2	Ylr113w	p27361	MAPK3	Mitogen-activated protein kinase 3/extracellular signal-regulated kinase 1
ygl158w	p51812	RPS6KA3	Ribosomal protein S6 kinase II alpha 3/insulin-stimulated protein kinase 1	Ylr113w	q15759	MAPK11	Mitogen-activated protein kinase 11
ygl158w	p53355	DAPIK1	Death-associated protein kinase 1/DAP-kinase 1	Ylr113w	p28482	MAPK1	Mitogen-activated protein kinase 1/extracellular signal-regulated kinase 2
ygl158w	q14012	CAMK1	Calcium/calmodulin-dependent protein kinase type I	Ylr113w	q16539	MAPK14	Mitogen-activated protein kinase 14/CsBP
ygl158w	q16566	CAMK4	calcium/calmodulin-dependent protein kinase IV	Ylr113w	q13164	MAPK7	Mitogen-activated protein kinase 7/ERK5
ygl158w	q16816	PHKG1	Phosphorylase B kinase gamma catalytic chain, skeletal muscle isoform	Ylr113w	p45984	MAPK9	Mitogen activated protein kinase 9
ygl189c	q06722	RPS26	Ribosomal protein S26	Ylr435w	p27797	CALR	Calreticulin/52kD ribonucleoprotein autoantigen RO/SS-A
ygl192w	p04062	G8A	Glucosylceramidase	Ybr057c	p49454	CENPF	CENP-F kinetochore protein

	p23511	NFYA	CAAT-box DNA binding protein subunit B	ybl021c	p25208	NFYB	CCAAT-binding factor subunit A/CAAT-box DNA binding protein subunit B
ygi237c	p54259	DRPLA	Atrophin-1/dentalobulbar-palidolusian atrophy protein	ybl021c	q01658	DR1	TATA binding protein-associated phosphoprotein
ygi242c	p20749	BCL3	B-cell lymphoma 3-encoded protein	ykr099w	p10244	MYBL2	Myb-related protein B/B-myb
ygi242c	p53355	DAPK1	Death-associated protein kinase 1/DAP-kinase 1	ykr099w	p10242	MYB	MYB proto-oncogene protein
ygi242c	q01484	ANK2	Ankyrin, brain variant 1/ankyrin B	ykr099w	p25054	APC	Adenomatous polyposis coli protein
ygi242c	q01485	ANK2	Brain ankyrin variant 2	ykr099w	p10243	MYBL1	Myb-related protein A/A-myb
ygi254w	p08151	GLI1	GLI protein/zinc finger protein GLI1	ygr047c	p19338	NCL	Nucleolin/protein C23
ygi254w	p41182	BCL6	B-cell lymphoma 6 protein/zinc finger protein 51	ygr047c	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM
ygi254w	p41182	BCL6	B-cell lymphoma 6 protein/zinc finger protein 51	yor039w	p13862	CSNK2B	Casikin kinase II beta subunit
ygr010w	q92764	KRTHA5	Keratin, type I cuticular HA5/hair keratin, type I HA5	ygr010w	q92764	KRTHA5	Keratin, type I cuticular HA5/hair keratin, type I HA5
ygr014w	p35658	NUP214	Nuclear pore complex protein NUP214/CAN protein	yil144w	p15924	DSP	Desmoplakin I and II
ygr014w	q02817	MUC2	Intestinal mucin 2/mucin 2	yil144w	q02224	CENPE	Centromeric protein E/CENP-E protein
ygr014w	q14157	KIAA0144	Hypothetical protein KIAA0144	yil144w	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform
ygr014w	q99102	MUC4	Tracheo-bronchial mucin 4/mucin 4 [fragment]	yil144w	p49454	CENPF	CENP-F kinetochore protein
ygr017w	p17480	UBTF	Nucleolar transcription factor 1/upstream binding factor 1/UBF-1	yir403w	q92785	REQ	Zinc-finger protein UBI-D4/apoptosis response zinc finger protein requiem
ygr058w	p07384	CAPN1	Calpain 1, large [catalytic] subunit/calcium activated neutral proteinase	ygr058w	p07384	CAPN1	Calpain 1, large [catalytic] subunit/calcium activated neutral proteinase
ygr058w	p17655	CAPN2	Ca2-activated neutral proteinase/calpain 2, Large [catalytic] subunit	ygr058w	p17655	CAPN2	Ca2-activated neutral proteinase/calpain 2, Large [catalytic] subunit
ygr058w	p20807	CAPN3	Calpain P94, large [catalytic] subunit/CANP	ygr058w	p20807	CAPN3	Calpain P94, large [catalytic] subunit/CANP
ygr058w	p28676	GCA	Grancalcin	ygr058w	p28676	GCA	Grancalcin
ygr058w	p30626	SRI	Sorcin	ygr058w	p30626	SRI	Sorcin
ygr058w	p07384	CAPN1	Calpain 1, large [catalytic] subunit/calcium activated neutral proteinase	ygr136w	p46108	CRK	Proto-oncogene C-CRK
ygr058w	p17655	CAPN2	Ca2-activated neutral proteinase/calpain 2, Large [catalytic] subunit	ygr136w	p06241	FYN	Proto-oncogene tyrosine-protein kinase FYN/SYN
ygr058w	p20807	CAPN3	Calpain P94, large [catalytic] subunit/CANP	ygr136w	p29354	GRB2	Growth factor receptor-bound protein 2
ygr058w	p28676	GCA	Grancalcin	ygr136w	p46109	CRKL	Crk-like protein
ygr058w	p30626	SRI	Sorcin	ygr136w	p14317	HCLS1	Hematopoietic lineage cell specific protein
ygr058w	p07384	CAPN1	Calpain 1, large [catalytic] subunit/calcium activated neutral proteinase	yir113w	q13164	MAPK7	Mitogen-activated protein kinase 7/ERK5
ygr058w	p17655	CAPN2	Ca2-activated neutral proteinase/calpain 2, Large [catalytic] subunit	yir113w	p53778	MAPK12	Mitogen-activated protein kinase 12/ERK6/extracellular signal-regulated kinase 6
ygr058w	p20807	CAPN3	Calpain P94, large [catalytic] subunit/CANP	yir113w	p45984	MAPK9	Mitogen activated protein kinase 9
ygr058w	p28676	GCA	Calpain P94, large [catalytic] subunit/CANP	yir113w	p28482	MAPK1	Mitogen-activated protein kinase 1/extracellular signal-regulated kinase 2
ygr058w	p30626	SRI	Sorcin	yir113w	p53779	MAPK10	Mitogen-activated protein kinase 10
ygr058w	p07384	CAPN1	Calpain 1, large [catalytic] subunit/calcium activated neutral proteinase	yni047c	q92636	NSMAF	Protein fan/factor associated with n-smase activation
ygr058w	p28676	GCA	Grancalcin	yni047c	q99418	ARNO	ARF nucleotide-binding site opener/ARNO protein/ARF exchange factor

ygr108w	p14635	CCNB1	G2/mitotic-specific cyclin B1	ybr135w	p10275	AR	Androgen receptor
ygr119c	p23490	LOR	Loricrin	ygl172w	p35658	NUP214	Nuclear pore complex protein NUP214/CAN protein
ygr119c	p35637	FUS	RNA-binding protein FUS/TLS	ygl172w	p49790	NUP153	Nuclear pore complex protein NUP153.
ygr119c	p35658	NUP214	Nuclear pore complex protein NUP214/CAN protein	ygl172w	p09651	HNRPA1	Heterogenous nuclear ribonucleoprotein A1/helix-destabilizing protein/single-strand binding protein/HNRNP core protein A1
ygr119c	p37198	NUP62	Nuclear pore glycoprotein P62	ygl172w	p23490	LOR	Loricrin
ygr119c	p49790	NUP153	Nuclear pore complex protein NUP153.	ygl172w	p52948	NUP98	Nuclear pore complex protein NUP98/Nucleoporin NUP98
ygr119c	p52948	NUP98	Nuclear pore complex protein NUP98/Nucleoporin NUP98	ygl172w	p13645	KRT10	Keratin, type I cytoskeletal 10
ygr119c	p23490	LOR	Loricrin	yj041w	q14093	CYLC2	Cylicin II
ygr119c	p35637	FUS	RNA-binding protein FUS/TLS	yj041w	p35663	CYLC1	Cylin I
ygr119c	p35658	NUP214	Nuclear pore complex protein NUP214/CAN protein	yj041w	p35658	NUP214	Nuclear pore complex protein NUP214/CAN protein
ygr119c	p37198	NUP62	Nuclear pore glycoprotein P62	yj041w	p37198	NUP62	Nuclear pore glycoprotein P62
ygr119c	p49790	NUP153	Nuclear pore complex protein NUP153.	yj041w	p49790	NUP153	Nuclear pore complex protein NUP153.
ygr119c	p52948	NUP98	Nuclear pore complex protein NUP98/Nucleoporin NUP98	yj041w	p52948	NUP98	Nuclear pore complex protein NUP98/Nucleoporin NUP98
ygr119c	p23490	LOR	Loricrin	yir423c	p15924	DSP	Desmoplakin I and II
ygr119c	p35637	FUS	RNA-binding protein FUS/TLS	yir423c	p49454	CENPF	CENP-F kinetochore protein
ygr119c	p35658	NUP214	Nuclear pore complex protein NUP214/CAN protein	yir423c	p30622	RSN	Reslin
ygr119c	p37198	NUP62	Nuclear pore glycoprotein P62	yir423c	q02224	CENPE	Centromeric protein E/CENP-E protein
ygr119c	p49790	NUP153	Nuclear pore complex protein NUP153.	yir423c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
ygr119c	p52948	NUP98	Nuclear pore complex protein NUP98/Nucleoporin NUP98	yir423c	p12270	TPR	Nucleoporin TPR
ygr119c	p37198	NUP62	Nuclear pore glycoprotein P62	Ymr236w	q16594	TAF2G	Transcription initiation factor TFIID 31 kD subunit
ygr144w	q16134	ETFDH	Electron transfer flavoprotein-ubiquinone oxidoreductase	ygr144w	q16134	ETFDH	Electron transfer flavoprotein-ubiquinone oxidoreductase
ygr155w	p35520	CBS	Cystathionine beta-synthase	ygr086w	p39880	CUTL1	CCAAT displacement protein/CDP
ygr229c	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	ykr099w	p10243	MYBL1	Myb-related protein A/A-myb
ygr229c	p46821	MAP1B	Microtubule-associated protein 1B	ykr099w	p25054	APC	Adenomatous polyposis coli protein
ygr229c	q05682	CALD1	Caldesmon/CDM	ykr099w	p10242	MYB	MYB proto-oncogene protein
ygr229c	q07283	THH	Trichohyalin	ykr099w	p10244	MYBL2	Myb-related protein B/B-myb
ygr250c	p11940	PABPL1	PolyA binding protein 1	yir001c	p26378	ELAVL4	Paraneoplastic encephalomyelitis antigen 3
ygr250c	p26378	ELAVL4	Paraneoplastic encephalomyelitis antigen 3	yir001c	q01844	EWSR1	RNA-binding protein EWS
ygr250c	p29558	RBMS1	Single-stranded DNA binding protein MSSP-1	yir001c	p35637	FUS	RNA-binding protein FUS/TLS
ygr250c	p33240	CSTF2	Cleavage stimulation factor, 64 kD subunit	yir001c	p33240	CSTF2	Cleavage stimulation factor, 64 kD subunit
ygr250c	p38159	HNRPG	Heterogeneous nuclear ribonucleoprotein G/HNRNP G/glycoprotein P43	yir001c	q01085	TIAL1	Nucleolysin TIAR
ygr250c	p98179	RBMS3	Putative RNA binding protein 3	yir001c	p11940	PABPL1	PolyA binding protein 1
ygr250c	q01085	TIAL1	Nucleolysin TIAR	yir001c	p08621	SNRP70	U1 small nuclear ribonucleoprotein 70kD
ygr250c	q15427	SAP49	Spliceosome associated protein 49/SAP49	yir001c	p98179	RBMS3	Putative RNA binding protein 3

	GCH1	p30793	ygr267c	GTP cyclohydrolase I		p30793	GCH1	GTP cyclohydrolase I
ygr267c	GCH1	p30793	ygr267c	GTP cyclohydrolase I		p30793	GCH1	GTP cyclohydrolase I
yhi004w	LAMR1	p08865	yhi004w	Colon carcinoma laminin-binding protein		q02224	CENPE	Centromeric protein E/CENP-E protein
yhi018w	PCBD	p80095	yhi018w	Pterin-4-alpha-carbinolamine dehydratase		p80095	PCBD	PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE
yhi019c	CLAPM1	p201172	yhi019c	Clathrin coat assembly protein AP47 homolog 2		p21851	CLAPB1	Beta adaptin
yhi019c	P47B	p53677	yhi019c	Clathrin coat assembly protein AP47 [fragment]		q10567	ADTB1	Beta-adaptin 1
yhi027w	SP1	p08047	yhi027w	Transcription factor SP1 [fragment]		p52745	ZNF36	Zinc finger protein 36/zinc finger protein KOX18
yhi027w	GLI1	p08151	yhi027w	GLI protein/zinc finger protein GLI1		p52740	ZNF132	Zinc finger protein 132
yhi027w	GLI2	p10070	yhi027w	Tax helper protein 2/zinc finger protein GLI2		p52736	ZNF133	Zinc finger protein 133
yhi027w	GLI3	p10071	yhi027w	Zinc finger protein GLI3		p52742	ZNF135	Zinc finger protein 135
yhi027w	EGR2	p11161	yhi027w	Early growth response protein 2/EGR-2		q15072	ZNF146	Zinc finger protein OZF
yhi027w	EGR1	p18146	yhi027w	Early growth response protein 1		q16600	ZNF239	Zinc finger protein 239/HOK-2
yhi027w	WT1	p19544	yhi027w	Wilms' tumor protein/WT33		p17032	ZNF37A	Zinc finger protein 37A [fragment]
yhi027w	ZNF43	p28160	yhi027w	Zinc finger protein 43/Zinc protein HTF6		q13360	ZNF177	Zinc finger protein 177
yhi027w	SP4	q02446	yhi027w	Transcription factor SP4/SPR-1		p51786	ZNF157	Zinc finger protein 157
yhi027w	EGR4	q05215	yhi027w	Early growth response protein 4		q06730	ZNF33A	Zinc finger protein 33A/KIAA0065
yhi027w	EGR3	q06889	yhi027w	Early growth response protein 3		q05516	ZNF145	Zinc finger protein PLZF/Zinc finger protein 145
yhr016c	FYN	p06241	yhr016c	Proto-oncogene tyrosine-protein kinase FYN/SYK		q03111	ENL	ENL protein
yhr016c	HCLS1	p14317	yhr016c	Hematopoietic lineage cell specific protein		p29375	RBBP2	RBBP-2/retnoblastoma binding protein 2
yhr016c	NCK	p16333	yhr016c	Cytoplasmic protein NCK		p11387	TOP1	Topoisomerase I
yhr016c	GRB2	p29354	yhr016c	Growth factor receptor-bound protein 2		p46821	MAP1B	Microtubule-associated protein 1B
yhr016c	CSK	p41240	yhr016c	Tyrosine-protein kinase CSK		p51825	MLLT2	AF-4 protein
yhr016c	SPTA2	q13813	yhr016c	Spectrin alpha chain, brain/nonerythroid alpha-spectrin		o14647	CHD2	Chromodomain-helicase-DNA-binding protein 2/CHD-2
yhr016c	ITSN	q15811	yhr016c	Intersectin/SH3 domain-containing protein SH3P17		p46939	UTRN	Utrophin
yhr039c	ALDH5	p30837	yhr039c	Mitochondrial aldehyde dehydrogenase X		p17931	LGALS3	Galectin-3/IgE-binding protein
yhr060w	PSMA4	p25789	yhr060w	Proteasome subunit C9		q02547	ATP6E	Vacuolar ATP synthase subunit AC39
yhr084w	POLR2A	p24928	yhr084w	DNA-directed RNA polymerase II largest subunit.		p17931	LGALS3	Galectin-3/IgE-binding protein
yhr108w	BPAG1	q03001	yhr108w	Bullous 230 kDa pemphigoid antigen 1		q02224	CENPE	Centromeric protein E/CENP-E protein
yhr111w	UBE1	p22314	yhr111w	Ubiquitin activating enzyme E1		p22314	UBE1	Ubiquitin activating enzyme E1
yhr111w	UBE1L	p41226	yhr111w	Ubiquitin-activating enzyme E1 homolog		p41226	UBE1L	Ubiquitin-activating enzyme E1 homolog
yhr114w	FES	p07332	yhr114w	C-FES/proto-oncogene tyrosine-protein kinase FES/FPS		p49454	CENPF	CENP-F kinetochore protein
yhr114w	TPR	p12270	yhr114w	Nucleoprotein TPR		p05787	KRT8	Keratin, type II cytoskeletal 8/cytokeratin 8/K8/CK8
yhr114w	MYH7	p12883	yhr114w	Myosin heavy chain, cardiac muscle beta isoform		p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
yhr114w	HCLS1	p14317	yhr114w	Hematopoietic lineage cell specific protein		p15924	DSN	Desmoplakin I and II
yhr114w	NCK	p16333	yhr114w	Cytoplasmic protein NCK		p30622	RSP	Reslin
yhr114w	FER	p16591	yhr114w	Tyrosine kinase FER		q02224	CENPE	Centromeric protein E/CENP-E protein
yhr114w	RGC1	p98171	yhr114w	RHO-GAP hematopoietic protein C1		p12270	TPR	Nucleoprotein TPR
yhr114w	CTTN	q14247	yhr114w	SRC substrate cortactin/amplixin		p11047	LAMC1	Laminin gamma-1 chain [precursor]/laminin B2 chain
yhr114w	ITSN	q15811	yhr114w	Intersectin/SH3 domain-containing protein SH3P17		q15431	SYCP1	Synaptonemal complex protein 1/SCP-1 protein
yhr143w-a	POLR2K	p53803	yhr143w-a	DNA-directed RNA polymerases I, II, and III 7.0 KD polypeptide		q02224	CENPE	Centromeric protein E/CENP-E protein
yhr171w	UBE1	p22314	yhr171w	Ubiquitin activating enzyme E1		p19338	NCL	Nudeoclin/protein C23

yhr204w	p33908	MA12	Mannosyl-oligosaccharide alpha-1,2-mannosidase	ygi030w	p04645	RPL30	Ribosomal protein L30
yji013c	p45844	ABCG1	White protein homolog	ydr174w	p09429	HMG1	High mobility group-1 protein
yji074c	p56545	CTBP2	C-terminal binding protein 2	yer081w	p56545	CTBP2	C-terminal binding protein 2
yji074c	q13363	CTBP1	C-terminal binding protein 1	ydr081w	q13363	CTBP1	C-terminal binding protein 1
yji074c	p56545	CTBP2	C-terminal binding protein 2	yji074c	p56545	CTBP2	C-terminal binding protein 2
yji074c	q13363	CTBP1	C-terminal binding protein 1	yji074c	q13363	CTBP1	C-terminal binding protein 1
yji105c	p20226	TBP	TATA-binding protein/transcription initiation factor	ydr179w	q14565	DMC1	Meiotic recombination protein DMC1/LIM15 homolog
yji105c	q93074	KIAA0192	TFIID	ydr179w	q06609	RAD51	DNA repair protein RAD51
yji105c	p20226	TBP	Hypothetical protein KIAA0192	yji047c	q99418	ARNO	ARF nucleotide-binding site opener/ARNO protein/ARF exchange factor
yji105c	q93074	KIAA0192	TFIID	yji047c	q92636	NSMAF	Protein fan/factor associated with n-s-mase activation
yji005w	p33240	CSTF2	Hypothetical protein KIAA0192	ygi174w	p35663	CYLC1	Cyclin I
yji036w	p08670	VIM	Cleavage stimulation factor, 64 kD subunit	yfr423c	p30622	RSN	Restin
yji036w	p12882	MYSS	Vimentin	yfr423c	p15924	DSP	Desmoplakin I and II
yji036w	p35580	MYH10	Myosin heavy chain skeletal muscle, light meromyosin region	yfr423c	p49454	CENPF	CENP-F kinetochore protein
yji036w	p35749	MYH11	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	yfr423c	p12270	TPR	Nucleoprotein TPR
yji036w	p48681	NES	Myosin heavy chain, smooth muscle isoform/SMMHC [FRAGMENT]	yfr423c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
yji036w	p49454	CENPF	Nestin	yfr423c	q02224	CENPE	Centromeric protein E/CENP-E protein
yji036w	q15036	KIAA0064	CENP-F kinetochore protein	yfr423c	q15431	SYCP1	Synaptonemal complex protein 1/SCP-1 protein
yji092w	p35580	MYH10	Hypothetical protein KIAA0064	ydr510w	p55854	SMT3H1	Ubiquitin-like protein SMT3A
yji092w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	ydr510w	p42568	MLLT3	AF-9 protein
yji110c	p23769	GATA2	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	ynl021w	q13547	HDAC1	Histone deacetylase 1/HD1
yji110c	p23771	GATA3	Endothelial transcription factor GATA-2	ynl021w	q92769	HDAC2	Histone deacetylase 2/HD2
yji110c	p43694	GATA4	Trans-acting T-cell specific transcription factor GATA-3	ynl021w	o15379	DHAC3	Histone deacetylase 3
yji110c	q92908	GATA6	Transcription factor GATA-4	ynl021w	p56524	KIAA0288	Hypothetical protein KIAA0288
yji112w	p11016	GNB2	Transcription factor GATA-6	yji001w	q05193	DNM1	Dynamin-1
yji112w	p43034	PAFAH1B1	Guanine nucleotide-binding protein beta subunit 2	yji001w	p20591	MX1	Interferon-regulated resistance GTP-binding protein MXA/Interferon-induced protein P78
yji112w	q12788	SAZD	Platelet-activating factor acetylhydrolase IB alpha subunit	yji001w	p50570	DNM2	Dynamin-2
yji112w	q15542	TAF2D	WD-repeat protein SAZD	yji001w	p20592	MX2	Interferon-regulated resistance GTP-binding protein MXB
yji137c	p46976	GYG	Transcription initiation factor TFIID 100 Kd subunit/TAFL-100/TAFL100	yji137c	p46976	GYG	Glycogenin-1
yji028w	p07199	CENP-B	Glycogenin-1	ydr311w	p32780	BTF2	Basic transcription factor 62kD subunit
yji028w	p07199	CENP-B	Major centromere autoantigen B/centromere protein B	ykr062w	p29084	GTF2E2	Transcription factor IIE beta subunit
yki067w	o00746	NME4	Major centromere autoantigen B/centromere protein B	yki067w	o00746	NME4	Nucleoside diphosphate kinase, mitochondrial
yki067w	p15531	NME1	Nucleoside-diphosphate kinase	yki067w	p15531	NME1	Nucleoside-diphosphate kinase A

yk1067w	p22392	NME2	Nucleoside diphosphate kinase B/NDP kinase B/nm23-H2	yk1067w	p22392	NME2	Nucleoside diphosphate kinase B/NDP kinase B/nm23-H2
yk1142w	p07942	LAMB1	Laminin beta-1 chain/Laminin B1 chain	yk1142w	p07942	LAMB1	Laminin beta-1 chain/Laminin B1 chain
yk1142w	p07942	LAMB1	Laminin beta-1 chain/Laminin B1 chain	Ymr165c	p51825	MLLT2	AF-4 protein
yk1166c	p14619	PRKG1	Type I beta cGMP-dependent protein kinase	yii033c	p10644	PRKAR1A	cAMP-dependent protein kinase regulatory subunit type I-alpha
yk1166c	p17612	PRKACA	cAMP-dependent protein kinase catalytic subunit type alpha	yii033c	q16281	CNCG3	CNCG3/cyclic nucleotide-gated cation channel 3 [fragment]
yk1166c	p22694	PRKACB	Testis-specific cAMP-dependent protein kinase catalytic subunit C-beta isoform	yii033c	q14028	CNG4	Cyclic-nucleotide-gated cation channel 4
yk1166c	p23443	RPS6KB1	P70 ribosomal S6 kinase alpha-II	yii033c	p29973	CNCG1	CGMP-gated cation channel protein/cyclic nucleotide-gated channel, photoreceptor/cyclic-nucleotide-gated cation channel1/CNG channel 1/CNG1/CNG-1
yk1166c	p24723	PRKCH	Protein kinase C, ETA type/protein kinase C-L	yii033c	p31321	PRKAR1B	cAMP-dependent protein kinase regulatory subunit RI-beta
yk1166c	p31749	AKT1	RAC-alpha serine/threonine kinase	yii033c	p13861	PRKAR2A	cAMP-dependent protein kinase type II-alpha regulatory chain
yk1166c	p31751	AKT2	RAC-beta serine/threonine kinase	yii033c	p31323	PRKAR2B	cAMP-dependent protein kinase subunit RI-beta
yk1166c	p51812	RPS6KA3	Ribosomal protein S6 kinase II alpha 3/Insulin-stimulated protein kinase 1	yii033c	p14619	PRKG1	Type I beta cGMP-dependent protein kinase
yk026c	p49770	EIF2B2	Translation initiation factor EIF-2B beta subunit/S20i115	Ykr026c	p49770	EIF2B2	Translation initiation factor EIF-2B beta subunit/S20i115
Ykr026c	q14232	ELF2B1	Translation initiation factor eIF-2B alpha subunit	Ykr026c	q14232	ELF2B1	Translation initiation factor eIF-2B alpha subunit
Ykr037c	p42566	EPS15	Epidermal growth factor receptor substrate 15	Ydr201w	p30622	RSN	Resilin
Ykr083c	p09429	HMG1	High mobility group-1 protein	Yk052c	p19338	NCL	Nucleolin/protein C23
Ykr083c	p17480	UBTF	Nucleolar transcription factor 1/upstream binding factor 1/UBF-1	Yk052c	q92794	MOZ	Monocytic leukemia zinc finger protein
Yl046c	p33240	CSTF2	Cleavage stimulation factor, 64 kD subunit	Yfr047c	q15274	NADC	Nicotinate-nucleotide pyrophosphorylase [carboxylating]/quinolinate phosphoribosyl transferase
Ylr200w	p49454	CENPF	CENP-F kinetochore protein	Ymr052w	p30622	RSN	Resilin
Ylr200w	q02224	CENPE	Centromeric protein E/CENP-E protein	Ymr052w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
Ylr216c	p05092	CYPA	Peptidyl-prolyl cis-trans isomerase A/cyclophilin A	Ylr037w	p36969	GPX4	Phospholipid hydroperoxide glutathione peroxidase/PHGPX
Ylr216c	p23284	PPIB	Peptidyl-prolyl C/S-trans isomerase B [precursor]/cyclophilin B	Ylr037w	p18283	GPX2	Glutathione peroxidase-GI.
Ylr216c	p30405	CYP3	Peptidyl-prolyl C/S-Trans isomerase/cyclophilin	Ylr037w	p12079	GPRP	Glutathione peroxidase-related protein 1
Ylr216c	p45877	PPIC	Peptidyl-prolyl cis-trans isomerase C/cyclophilin C	Ylr037w	p22352	GPX3	Plasma glutathione peroxidase
Ylr216c	q08752	PPID	40 kD peptidyl-prolyl C/S-TRANS isomerase/cyclophilin-40 mRNA, complete cds.	Ylr037w	p07203	GPX1	Glutathione peroxidase
Ylr229c	p21181	CDC42	G25K GTP-binding protein	Ydl135c	p52565	ARHGDI A	Rho GDP-dissociation Inhibitor 1.
Ylr229c	p25763	CDC42	GTP-binding protein G25K, placental isoform	Ydl135c	p52566	ARHGDI B	Rho GDP-dissociation inhibitor 2
Ylr245c	p32320	CDA	Cytidine deaminase	Ylr245c	p32320	CDA	Cytidine deaminase
Ylr305c	p42336	PIK3CA	Phosphatidylinositol 3-kinase catalytic subunit, alpha	Yor355w	q14669	TRIP12	Thyroid receptor interacting protein 12/KIAA0045

yfr4305c	p42345	FRAP	isoform	yfr355w	p42568	MLLT3	AF-9 protein
yfr423c	p15924	DSP	FKBP-rapamycin associated protein	ygr120c	p30622	RSN	Restin
yfr423c	p49454	CENPF	Desmoplakin I and II	ygr120c	p49454	CENPF	CENP-F kinetochore protein
yfr423c	q02224	CENPE	CENP-F kinetochore protein	ygr120c	p04114	APOB	Apolipoprotein B
yfr423c	p05787	KRT8	Centromeric protein E/CENP-E protein	yfr423c	p05787	KRT8	Keratin, type II cytoskeletal 8/cytokeratin 8/K8/CK8
yfr423c	p11047	LAMC1	Keratin, type II cytoskeletal 8/cytokeratin 8/K8/CK8	yfr423c	p11047	LAMC1	Laminin gamma-1 chain [precursor]/laminin B2 chain
yfr423c	p12270	TPR	Laminin gamma-1 chain [precursor]/laminin B2 chain	yfr423c	p12270	TPR	Nucleoporin TPR
yfr423c	p13535	MYH8	Nucleoporin TPR	yfr423c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
yfr423c	p15924	DSP	Myosin heavy chain, perinatal skeletal muscle	yfr423c	p15924	DSP	Desmoplakin I and II
yfr423c	p30622	RSN	Desmoplakin I and II	yfr423c	p30622	RSN	Restin
yfr423c	p49454	CENPF	Restin	yfr423c	p49454	CENPF	CENP-F kinetochore protein
yfr423c	q02224	CENPE	CENP-F kinetochore protein	yfr423c	q02224	CENPE	Centromeric protein E/CENP-E protein
yfr423c	q15431	SYCP1	Centromeric protein E/CENP-E protein	yfr423c	q15431	SYCP1	Synaptonemal complex protein 1/SCP-1 protein
yfr424w	p49454	CENPF	Synaptonemal complex protein 1/SCP-1 protein	yfr422c	p49454	CENPF	CENP-F kinetochore protein
yfr424w	p52756	LUCA15	CENP-F kinetochore protein	yfr422c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
yfr424w	p98175	DXS8237E	Putative tumor suppressor LUCA15	yfr422c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMHC-B
			DXS8237E protein				Major centromere autoantigen B/centromere protein B
yfr429w	p31146	CORO1	Coronin-like Protein p57	ydr328c	p07199	CENP-B	Cyclin ACDK2-associated p19
yfr429w	p43034	PAFAH1B1	Platelet-activating factor acetylhydrolase IB alpha subunit	ydr328c	p34991	TCEB1L	Nucleolar transcription factor 1/upstream binding factor 1/UBF-1
yfr429w	p46821	MAP1B	Microtubule-associated protein 1B	ydr328c	p17480	UBTF	Nucleolin/protein C23
yfr429w	q16576	RBBP7	Histone acetyl transferase type B subunit	ydr328c	p19338	NCL	Transcription initiation factor TFIID 30 Kd subunit/TAFII-30/TAFII30
yfr432w	p12268	IMPDH2	2/retnoblastoma-binding protein	ydr167w	q12962	TAF2H	Translation initiation factor eIF-2B alpha subunit
yfr432w	p12268	IMPDH2	Inosine monophosphate dehydrogenase 2	ykr026c	q14232	ELF2B1	Translation initiation factor EIF-2B beta subunit/S20i115
yfr432w	p20839	IMPDH1	Inosine-5'-monophosphate dehydrogenase 1/IMP dehydrogenase 1/IMPDH-1/IMPDH	ykr026c	p49770	EIF2B2	ARF nucleotide-binding site opener/ARNO protein/ARF exchange factor
yfr433c	p05323	PPP2CA	Serine/threonine protein phosphatase PP2A-alpha, catalytic subunit	ynl047c	q99418	ARNO	Protein fan/factor associated with n-smase activation
yfr433c	q08209	PPP3CA	Serine/threonine protein phosphatase 2B catalytic subunit. Alpha isoform/calmodulin-dependent calcineurin A subunit, alpha subunit	ynl047c	q92636	NSMAF	Keratin, type I cuticular HA5/hair keratin, type I HA5
yfr438w	p04181	OAT	Ornithine aminotransferase	ygr010w	q92764	KRTHA5	TATA-binding protein/transcription initiation factor TFIID
yfr438w	p04181	OAT	Ornithine aminotransferase	yhl025w	p20226	TBP	Transcription initiation factor TFIID 30 Kd subunit/TAFII-30/TAFI30
ynl015c	p52655	GTF2A1	Transcription initiation factor IIA alpha and beta chains/TFIIA-42	ydr167w	q12962	TAF2H	High mobility group-1 protein
ynl015c	p52655	GTF2A1	Transcription initiation factor IIA alpha and beta chains/TFIIA-42	ydr174w	p09429	HMG1	High mobility group protein HMG2/HMG-2
ynl015c	q15544	TAF2I	Transcription initiation factor TFIID 28 KD subunit	ydr174w	p26583	HMG2	

ymr088w	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	ydr328c	p07199	CENP-B	Major centromere autoantigen B/centromere protein B
ymr094w	p49454	CENPF	CENP-F kinetochore protein	yfr200w	q02224	CENPE	Centromeric protein E/CENP-E protein
ymr094w	q99471	MM-1	C-myc binding protein MM-1	yfr200w	p49454	CENPF	CENP-F kinetochore protein
ymr114c	q02832	BLSA	B-lymphocyte antigen/B-lymphocyte surface antigen	ydr167w	q12962	TAF2H	Transcription initiation factor TFIIID 30 Kd subunit/TAFLI-30/TAFLI30
ymr032w	p02533	KRT14	Keratin, type I cytoskeletal 14	yfr423c	p49454	CENPF	CENP-F kinetochore protein
ymr032w	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	yfr423c	q02224	CENPE	Centromeric protein E/CENP-E protein
ymr052w	p30622	RSN	Resilin	yfr008w	p12270	TPR	Nucleoprotein TPR
ymr052w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type BINMMHC-B	yfr008w	q02224	CENPE	Centromeric protein E/CENP-E protein
ymr068w	p20749	BCL3	B-cell lymphoma 3-encoded protein	yfr105c	q10571	MN1	Probable tumor suppressor protein MN1
ymr068w	q01484	ANK2	Ankyrin, brain variant 1/ankyrin B	yfr105c	p20226	TBP	TATA-binding protein/transcription initiation factor TFIIID
ymr068w	q01485	ANK2	Brain ankyrin variant 2	yfr105c	q93074	KIAA0192	Hypothetical protein KIAA0192
ymr077c	p12270	TPR	Nucleoprotein TPR	yfr052c	p19338	NCL	Nucleolin/protein C23
ymr077c	p35579	MYH9	Myosin heavy chain, nonmuscle type A/cellular myosin heavy chain, type ANMMHC-A	yfr052c	q92794	MOZ	Monocytic leukemia zinc finger protein
ymr091c	p07199	CENP-B	Major centromere autoantigen B/centromere protein B	yfr037c	q15431	SYCP1	Synaptonemal complex protein 1/SCP-1 protein
ymr093w	q14727	APAF1	Apoptotic protease activating factor 1/APAF-1	ydr398w	p17480	UBTF	Nuclear transcription factor 1/upstream binding factor 1/UBF-1
ymr093w	p25388	GNB2-RS1	Guanine nucleotide-binding protein beta subunit-like protein 12.3	ydr398w	p07199	CENP-B	Major centromere autoantigen B/centromere protein B
ymr093w	p35606	COPP	Beta subunit of coatomer complex	ydr398w	p27824	CANX	Calnexin/JP90
ymr093w	q13610	PWP1	Periodic tryptophan protein 1 homolog/keratinocyte protein IEF SSP 9502	ydr398w	p39687	PHAP1	HLA-DR associated protein I
ymr093w	q15542	TAF2D	Transcription initiation factor TFIIID 100 kD subunit/TAFLI-100/TAFLI100	ydr398w	q01105	SET	Set protein/ HLA-DR associated protein II/PHAPII
ymr102c	p25388	GNB2-RS1	Guanine nucleotide-binding protein beta subunit-like protein 12.3	ynl218w	p35249	RFC4	Activator 1 37 kD subunit/replication factor C, 37-kDa subunit
ymr102c	p43034	PAFAH1B1	Platelet-activating factor acetylhydrolase IB alpha subunit	ynl218w	p35250	RFC2	Activator 1 40 kD subunit/replication factor C, 40 kDa subunit
ymr102c	p53621	COPA	Coatomer alpha subunit	ynl218w	p40937	RFC5	Activator 1 36 kD subunit/replication factor C, 36-kDa subunit
ymr102c	q13610	PWP1	Periodic tryptophan protein 1 homolog/keratinocyte protein IEF SSP 9502	ynl218w	p35251	RFC1	Replication factor C large subunit/activator 1140 Kd subunit
ymr210w	p08910	PHS1-2	PHS1-2 with ORF homologous to membrane receptor proteins	yfr142w	p07942	LAMB1	Laminin beta-1 chain/Laminin B1 chain
ymr212c	q14156	KIAA0143	Hypothetical protein KIAA0143	yfr423c	q02224	CENPE	Centromeric protein E/CENP-E protein
ymr255w	q14647	CHD2	Chromodomain-helicase-DNA-binding protein 2/CHD-2	yfr122c	q92794	MOZ	Monocytic leukemia zinc finger protein
ymr255w	p11387	TOP1	Topoisomerase I	yfr122c	q93074	KIAA0192	Hypothetical protein KIAA0192
ymr255w	p29375	RBBP2	RBBP-2/retinoblastoma binding protein 2	yfr122c	p20226	TBP	TATA-binding protein/transcription initiation factor TFIIID
ymr255w	p46821	MAP1B	Microtubule-associated protein 1B	yfr122c	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM

ymr255w	p46939	UTRN	Ulrophin	ygl122c	q10571	MN1	Probable tumor suppressor protein MN1
ymr255w	p51825	MILLT2	AF-4 protein	ygl122c	p42858	HD	Huntinglin/huntington's disease protein
ymr255w	q03111	ENL	ENL protein	ygl122c	q14814	MEF2D	Myocyte-specific enhancer factor 2D
ymr267w	q15181	PP	Inorganic pyrophosphatase [fragment]/Ppase	ykr026c	q14232	ELF2B1	Translation initiation factor eIF-2B alpha subunit
ymr269w	p35863	CYLC1	Cyclin I	ykr026c	q14232	ELF2B1	Translation initiation factor eIF-2B alpha subunit
ymr269w	q14093	CYLC2	Cyclin II	ykr026c	p49770	EIF2B2	Translation initiation factor eIF-2B beta subunit/S20i115
ymr309c	p17480	UBTF	Nucleolar transcription factor 1/upstream binding factor 1/UBF-1	ynl047c	q92636	NSMAF	Protein fan/factor associated with n-smase activation
ymr309c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular	ynl047c	q99418	ARNO	ARF nucleotide-binding site opener/ARNO protein/ARF exchange factor
ymr309c	p35580	MYH10	myosin heavy chain, type B/NNMMHC-B	ynl244c	p41567	SUI1	Protein translation factor SUI1 homolog/sui1iso1
ynl023c	p35555	FBN1	myosin heavy chain, nonmuscle type B/cellular	Ymr224c	p49959	MRE11A	Double-strand break repair protein MRE11A/MRE11 homolog
ynl078w	p18583	SON	Fibrillin 1 [precursor]	ykr048c	p55209	NAP1L1	NAP-1/nucleosome assembly protein 1-like 1
ynl091w	q02832	BLSA	Son protein/son3	ynl164c	q13190	STX5A	Syntaxin 5
ynl091w	p46821	MAP1B	B-lymphocyte antigen/B-lymphocyte surface antigen	ykr355w	q14669	TRIP12	Thyroid receptor interacting protein 12/KIAA0045
ynl091w	q02832	BLSA	Microtubule-associated protein 1B	ykr355w	p42568	MLLT3	AF-9 protein
ynl091w	p23327	HRC	B-lymphocyte antigen/B-lymphocyte surface antigen	ypl229w	p20265	POU3F2	Nervous-system specific octamer-binding transcription factor N-Oct 3/N-Oct 5a/N-Oct 5b
ynl091w	p35579	MYH9	Sarcoplasmic reticulum histidine-rich calcium binding protein	ypl229w	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM
ynl091w	p35749	MYH11	Myosin heavy chain, nonmuscle type A/cellular	ypl229w	q93074	KIAA0192	Hypothetical protein KIAA0192
ynl091w	p45379	TNNT2	myosin heavy chain, type A/NNMMHC-A	ypl229w	q01826	SATB1	DNA binding protein SATB1
ynl091w	p46100	ATRX	Myosin heavy chain, smooth muscle isoform/SMMHC [FRAGMENT]	ypl229w	p54252	MJD1	Machado-joseph disease protein 1
ynl091w	p46821	MAP1B	Troponin T, cardiac muscle isoforms	ypl229w	p42858	HD	Huntinglin/huntington's disease protein
ynl091w	q02832	BLSA	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	ypl229w	p10275	AR	Androgen receptor
ynl091w	q05682	CALD1	Microtubule-associated protein 1B	ypl229w	q10571	MN1	Probable tumor suppressor protein MN1
ynl091w	q07283	THH	B-lymphocyte antigen/B-lymphocyte surface antigen	ypl229w	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID
ynl091w	q15696	U2AF1-RS2	Caldesmon/CDM	ypl229w	p54253	SCA1	Ataxin-1/Spinocerebellar ataxia type 1 protein
ynl127w	p20309	CHRM3	Trichohyalin	ypl229w	p30153	PPP2R1A	Protein phosphatase PP2A, 65Kd regulatory subunit alpha-isotype
ynl127w	p20309	CHRM3	U2 small nuclear ribonucleoprotein auxiliary factor 35 kD subunit related-protein 2	ykr055w	p21181	CDC42	G25K GTP-binding protein
ynl154c	p48729	CSNK1A1	Muscarinic acetylcholine receptor M3	ydc054w	q05682	CALD1	Caldesmon/CDM
ynl154c	p48730	CSNK1D	Muscarinic acetylcholine receptor M3	ydc054w	p35663	CYLC1	Cyclin I
ynl154c	p49674	CSNK1E	Casein kinase I, alpha isoform/CKI-alpha/CK1	ydc054w	p12883	MYH7	MYOSIN, CARDIAC, HEAVY CHAIN, BETA
ynl154c	p51812	RPS6KA3	Casein kinase I delta isoform	ydc054w	p19338	NCL	Nucleolin/protein C23
ynl154c	p78368	CSNK1G2	Casein kinase I epsilon	ydc054w	p35579	MYH9	Myosin heavy chain, nonmuscle type A/cellular myosin heavy chain, type A/NNMMHC-A
ynl154c	p78368	CSNK1G2	Ribosomal protein S6 kinase II alpha 3/insulin-simulated protein kinase 1				
ynl154c	p78368	CSNK1G2	Casein kinase I, gamma 2 isoform				

ynl154c	p48730	CSNK1D	Casein kinase I delta isoform	ycr011c	p45844	ABCG1	White protein homolog
ynl154c	p48729	CSNK1A1	Casein kinase I, alpha isoform/CKI-alpha/CK1	yki204w	p10163	PRB4	PROLINE-RICH PROTEIN, BsINI SUBFAMILY, 4
ynl154c	p48730	CSNK1D	Casein kinase I delta isoform	yki204w	p48634	BAT2	Large proline-rich protein BAT2/HLA-B-associated transcript 2
ynl154c	p49674	CSNK1E	Casein kinase I epsilon	yki204w	p54259	DRPLA	Atrophin-1/dentatorubral-pallidoluysian atrophy protein
ynl154c	p51812	RPS6KA3	Ribosomal protein S6 kinase II alpha 3/insulin-stimulated protein kinase 1	yki204w	p04280	PRB1	Salivary proline-rich protein/clone CP3, CP4, and CP5
ynl154c	p78368	CSNK1G2	Casein kinase I, gamma 2 isoform	yki204w	p02812	PRB2	Salivary proline-rich protein/Clone CP7
ynl154c	p48730	CSNK1D	Casein kinase I delta isoform	Ymr267w	q15181	PP	Inorganic pyrophosphatase [fragment]/Ppase
ynl154c	p48730	CSNK1D	Casein kinase I delta isoform	yor355w	p42568	MLLT3	AF-9 protein
ynl154c	p49674	CSNK1E	Casein kinase I epsilon	yor355w	q14669	TRIP12	Thyroid receptor interacting protein 12/KIAA0045
ynl189w	p35222	CTNNB1	Beta-catenin.	ybr252w	p33316	DUT	Deoxyuridine triphosphatase nucleotidohydrolase
ynl189w	p52294	KPNA1	Importin alpha-1 subunit/SRP1-beta/nucleoprotein interactor 1	ybr252w	p10265	PRT	Retrovirus-related protease
ynl189w	o00505	KPNA3	Karyopherin alpha 3	yh1009c	p17861	XBP1	X box binding protein-1/XBP-1
ynl189w	o00629	QIP1	Karyopherin alpha 4/Qip1	yh1009c	q15431	SYCP1	Synaptonemal complex protein 1/SCP-1 protein
ynl189w	p35222	CTNNB1	Beta-catenin.	yh1009c	p25054	APC	Adenomatous polyposis coli protein
ynl189w	p52292	KPNA2	Importin alpha-2 subunit/SRP1-alpha	yh1009c	p12270	TPR	Nucleoprotein TPR
ynl189w	p52294	KPNA1	Importin alpha-1 subunit/SRP1-beta/nucleoprotein interactor 1	yh1009c	q02224	CENPE	Centromeric protein E/CENP-E protein
ynl189w	p35222	CTNNB1	Beta-catenin.	yjr159w	p11766	ADH5	Class III alcohol dehydrogenase chi subunit
ynl189w	p52294	KPNA1	Importin alpha-1 subunit/SRP1-beta/nucleoprotein interactor 1	yjr159w	q00796	SORD	Sorbitol dehydrogenase/L-idoitol-2 dehydrogenase
ynl189w	p35222	CTNNB1	Beta-catenin.	yjr303w	p32929	CTH	Cystathionine gamma-lyase
ynl189w	o00505	KPNA3	Karyopherin alpha 3	ymi028w	p32119	TDPX1	Thioredoxin peroxidase 1/thioredoxin-dependent peroxide reductase 1/thiol-specific antioxidant protein/TSA/PRP/natural killer cell enhancing factor B/NKEF-B
ynl189w	o00629	QIP1	Karyopherin alpha 4/Qip1	ymi028w	q13162	AOE372	Thioredoxin peroxidase AO372/antioxidant enzyme AOE372
ynl189w	p35222	CTNNB1	Beta-catenin.	ymi028w	q06830	TDPX2	Thioredoxin peroxidase 2/proliferation-associated gene (pag).
ynl189w	p52292	KPNA2	Importin alpha-2 subunit/SRP1-alpha	ymi028w	p30041	AOP2	Antioxidant protein 2
ynl189w	p52294	KPNA1	Importin alpha-1 subunit/SRP1-beta/nucleoprotein interactor 1	ymi028w	p30048	AOP1	Mitochondrial thioredoxin-dependent peroxide reductase/antioxidant protein 1
ynl189w	o00505	KPNA3	Karyopherin alpha 3	Ymr226c	p15428	PGDH1	15-Hydroxyprostaglandin dehydrogenase [NAD(+)]/PGDH
ynl189w	p35222	CTNNB1	Beta-catenin.	Ymr226c	q02338	BDH	D-beta-hydroxybutyrate dehydrogenase/3-hydroxybutyrate dehydrogenase
ynl189w	p52292	KPNA2	Importin alpha-2 subunit/SRP1-alpha	Ymr226c	q92781	RDH1	11-ds retinol dehydrogenase
ynl189w	p52294	KPNA1	Importin alpha-1 subunit/SRP1-beta/nucleoprotein interactor 1	Ymr226c	p14061	E2DH	Estradiol 17 beta-dehydrogenase
ynl189w	p35222	CTNNB1	Beta-catenin.	yo1058w	p00966	ASS	Argininosuccinate synthase/citrulline-aspartate ligase
ynl189w	p35222	CTNNB1	Beta-catenin.	yp1111w	p78540	ARG2	Arginase II/non-hepatic arginase

ynl189w	p52294	KPNA1	Importin alpha-1 subunit/SRP1-beta/nucleoprotein interactor 1	yp1111w	p05089	ARG1	Arginase 1
ynl210w	q00341	HBP	High density lipoprotein binding protein	yk1142w	p07942	LAMB1	Laminin beta-1 chain/Laminin B1 chain
ynl218w	p35249	RFC4	Activator 1 37 kD subunit/replication factor C, 37-kDa subunit	ylr423c	p49454	CENPF	CENP-F kinetochore protein
ynl218w	p35250	RFC2	Activator 1 40 kD subunit/replication factor C, 40 kDa subunit	ylr423c	p15924	DSP	Desmoplakin I and II
ynl218w	p35251	RFC1	Replication factor C large subunit/activator 1140 Kd subunit	ylr423c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
ynl218w	p40937	RFC5	Activator 1 36 kD subunit/replication factor C, 36-kDa subunit	ylr423c	q02224	CENPE	Centromeric protein E/CENP-E protein
ynl218w	p35249	RFC4	Activator 1 37 kD subunit/replication factor C, 37-kDa subunit	ynl218w	p35249	RFC4	Activator 1 37 kD subunit/replication factor C, 37-kDa subunit
ynl218w	p35250	RFC2	Activator 1 40 kD subunit/replication factor C, 40 kDa subunit	ynl218w	p35250	RFC2	Activator 1 40 kD subunit/replication factor C, 40 kDa subunit
ynl218w	p35251	RFC1	Replication factor C large subunit/activator 1140 Kd subunit	ynl218w	p35251	RFC1	Replication factor C large subunit/activator 1140 Kd subunit
ynl218w	p40937	RFC5	Activator 1 36 kD subunit/replication factor C, 36-kDa subunit	ynl218w	p40937	RFC5	Activator 1 36 kD subunit/replication factor C, 36-kDa subunit
ynl287w	p21851	CLAPB1	Beta adaptin	ybr281c	p31146	CORO1	Coronin-like Protein P57
ynl287w	q10567	ADTB1	Beta-adaptin 1	ybr281c	p35806	COPP	Beta subunit of coatomer complex
ynr006w	p12036	NEFH	Neurofilament triplet H protein/200 Kd neurofilament protein	yh1002w	q15811	ITSN	Intersectin/SH3 domain-containing protein SH3P17
ynr006w	p26358	DNMT	DNA/cytosine-5)methyl transferase/DNA methyltransferase/DNA methylase/MCMT/MLHSAI	yh1002w	q14247	CTTN	SRC substrate contactin/ampixin
ynr006w	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	yh1002w	p19174	PLCG1	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma 1/phospholipase C-gamma 1
ynr006w	p80303	NEFA	DNA binding protein NEFA	yh1002w	p16333	NCK	Cytoplasmic protein NCK
ynr006w	p98174	FGD1	Putative RHO/RAC guanine nucleotide exchange factor/faciogenital dysplasia protein	yh1002w	p14317	HCLS1	Hematopoietic lineage cell specific protein
ynr006w	q02224	CENPE	Centromeric protein E/CENP-E protein	yh1002w	p29354	GRB2	Growth factor receptor-bound protein 2
ynr006w	q07283	THH	Trichohyalin	yh1002w	p98171	RGC1	RHO-GAP hematopoietic protein C1
ynr006w	q13438	OS9	Protein OS-9 precursor	yh1002w	p46109	CRKL	Crk-like protein
ynr006w	q92794	MOZ	Monocytic leukemia zinc finger protein	yh1002w	q13813	SPTA2	Spectrin alpha chain, brain/nonerythroid alpha-spectrin
yo1034w	p11055	MYH3	Embryonic myosin heavy chain.	Ymr117c	p04264	KRT1	Keratin, type II cytoskeletal 1/cytokeratin 1/K1/CK1/67Kd cytokeratin/hair alpha protein
yo1034w	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform	Ymr117c	p30622	RSN	Resilin
yo1034w	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	Ymr117c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
yo1034w	p15924	DSP	Desmoplakin I and II	Ymr117c	p11055	MYH3	Embryonic myosin heavy chain.
yo1034w	p49454	CENPF	CENP-F kinetochore protein	Ymr117c	p42566	EPS15	Epidermal growth factor receptor substrate 15
yo1034w	q02224	CENPE	Centromeric protein E/CENP-E protein	Ymr117c	p49454	CENPF	CENP-F kinetochore protein
yo1059w	p21695	GPD1	L-glycerol-3-phosphate dehydrogenase [NAD+]	Yl017c	p08578	SNRPE	Small nuclear ribonucleoprotein E/snRNP-E

yo1061w	p09329	PRPS1	Phosphoribosyl pyrophosphate synthetase I/ribose-phosphate pyrophosphokinase I	yer099c	p09329	PRPS1	Phosphoribosyl pyrophosphate synthetase I/ribose-phosphate pyrophosphokinase I
yo1061w	p11908	PRPS2	Phosphoribosyl pyrophosphate synthetase subunit II	yer099c	p11908	PRPS2	Phosphoribosyl pyrophosphate synthetase subunit II
yo1061w	p21108	PRPS3	Phosphoribosyl pyrophosphate synthetase subunit III	yer099c	p21108	PRPS3	Phosphoribosyl pyrophosphate synthetase subunit III
yo1069w	p15924	DSP	Desmoplakin I and II	yer099c	p15924	DSP	Desmoplakin I and II
yo1069w	p49454	CENPF	CENP-F kinetochore protein	yer099c	p49454	CENPF	CENP-F kinetochore protein
yo1069w	q02224	CENPE	Centromeric protein E/CENP-E protein	yer099c	q02224	CENPE	Centromeric protein E/CENP-E protein
yo1069w	p12270	TPR	Nucleoprotein TPR	yfr423c	p05787	KRT8	Keratin, type II cytoskeletal 8/cytokeratin 8/K8/CK8
yo1069w	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform	yfr423c	p30622	RSN	Restin
yo1069w	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	yfr423c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
yo1069w	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle	yfr423c	q15431	SYCP1	Synaptonemal complex protein 1/SCP-1 protein
yo1069w	p15924	DSP	Desmoplakin I and II	yfr423c	p15924	DSP	Desmoplakin I and II
yo1069w	p30622	RSN	Restin	yfr423c	p11047	LAMC1	Laminin gamma-1 chain (precursor)/laminin B2 chain
yo1069w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMHC-B	yfr423c	p12270	TPR	Nucleoprotein TPR
yo1069w	p49454	CENPF	CENP-F kinetochore protein	yfr423c	p49454	CENPF	CENP-F kinetochore protein
yo1069w	q02224	CENPE	Centromeric protein E/CENP-E protein	yfr423c	q02224	CENPE	Centromeric protein E/CENP-E protein
yo1088c	p13667	ERP72	Protein disulfide isomerase related protein/ERP72	yhr091c	p54136	RARS	ArgRS/arginyl-tRNA synthetase
yo1088c	q02505	MUC3	Mucin 3 [fragments]/intestinal mucin 3	ygl153w	q02224	CENPE	Centromeric protein E/CENP-E protein
yo1105c	q99102	MUC4	Tracheo-bronchial mucin 4/mucin 4 [fragment]	ygl153w	q03001	BPAG1	Bullous 230 kDa pemphigoid antigen 1
yo1108c	p98171	RGC1	RHO-GAP hematopoietic protein C1	yk017c	p38935	IGHMBP2	DNA-binding protein SMBP2
yo1108c	p98171	RGC1	RHO-GAP hematopoietic protein C1	yk135c	q10567	ADTB1	Beta-adaptin 1
yo1108c	p98171	RGC1	RHO-GAP hematopoietic protein C1	ymr317w	q02817	MUC2	Intestinal mucin 2/mucin 2
yo1111c	p11441	GDX	Ubiquitin-like protein GDX	yor007c	p50502	HIP	Progesterone receptor-associated p48 protein
yo1111c	p54725	RAD23A	UV excision repair protein RAD23 homolog A/HHR23A	yor007c	p30260	CDC27	Protein CDC27HS/cell division cycle protein 27 homolog
yo1111c	p54727	D21090	UV excision repair protein RAD23 homolog B/XPC-C repair complementing protein (p58/HHR23B), complete cds.	yor007c	q08752	PPID	40 kD peptidyl-prolyl CIS-TRANS isomerase/cyclophilin-40 mRNA, complete cds.
yo1123w	p07029	UP2	Heterogeneous nuclear ribonucleoprotein UP2	ygl122c	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID
yo1123w	p09651	HNRPA1	Heterogeneous nuclear ribonucleoprotein A1/helix-destabilizing protein/single-strand binding protein/HNRNP core protein A1	ygl122c	q10571	MN1	Probable tumor suppressor protein MN1
yo1123w	p11940	PABPL1	PolyA binding protein 1	ygl122c	q14814	MEF2D	Myocyte-specific enhancer factor 2D
yo1123w	p22626	HNRPA2B1	Heterogeneous nuclear ribonucleoproteins A2/B1	ygl122c	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM
yo1123w	p26378	ELAVL4	Paraneoplastic encephalomyelitis antigen 3	ygl122c	p42858	HD	Huntingtin/huntington's disease protein
yo1123w	p38159	HNRPG	Heterogeneous nuclear ribonucleoprotein G/HNRNP G/glycoprotein P43	ygl122c	q92794	MOZ	Monocytic leukemia zinc finger protein
yo1123w	q15427	SAP49	Spliceosome associated protein 49/SAP49	ygl122c	q93074	KIAA0192	Hypothetical protein KIAA0192
yo1130w	p46821	MAP1B	Microtubule-associated protein 1B	ygl025c	q02078	MEF2A	Myocyte-specific enhancer factor 2A
yo1130w	q04724	TLE1	Transducin-like enhancer protein	ygl025c	q02817	MUC2	Intestinal mucin 2/mucin 2
yo1130w	p46821	MAP1B	Microtubule-associated protein 1B	yfr291c	q14232	ELF2B1	Translation initiation factor eIF-2B alpha subunit
yo1130w	q04724	TLE1	Transducin-like enhancer protein	yfr291c	p49770	EIF2B2	Translation initiation factor eIF-2B beta subunit/S20iii15

yor061w	p24941	CDK2	Cell division protein kinase 2	yor039w	p13862	CSNK2B	Casein kinase II beta subunit
yor128c	p22234	PAICS	ADE2 showing homologies to SAICAR synthetase and AIR carboxylase of the purine pathway	yor066w	p35226	BMI1	DNA-binding protein BMI1
yor128c	p22234	PAICS	ADE2 showing homologies to SAICAR synthetase and AIR carboxylase of the purine pathway	yor067c	p42568	MLLT3	AF-9 protein
yor128c	p22234	PAICS	ADE2 showing homologies to SAICAR synthetase and AIR carboxylase of the purine pathway	yor128c	p22234	PAICS	ADE2 showing homologies to SAICAR synthetase and AIR carboxylase of the purine pathway
yor132w	q00839	HNRNPU	ADE2 showing homologies to SAICAR synthetase and AIR carboxylase of the purine pathway	yor069w	q12840	KIF5C	Neuronal kinesin heavy chain
yor269w	p25388	GNB2-RS1	Heterogenous nuclear ribonucleoprotein U/scaffold attachment factor A	ylr254c	p49454	CENPF	CENP-F kinetochore protein
yor269w	p35606	COPP	Guanine nucleotide-binding protein beta subunit-like protein 12.3	ylr254c	q02224	CENPE	Centromeric protein E/CENP-E protein
yor269w	p43034	PAFAH1B1	Beta subunit of coatomer complex	ylr254c	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform
yor303w	p31327	CPS1	Platelet-activating factor acetylhydrolase IB alpha subunit	yor039w	p13862	CSNK2B	Casein kinase II beta subunit
yor348c	p52569	SLC7A2	Carbamoyl-phosphate synthase [ammonia], mitochondrial [precursor]	yor045c	p29144	TTP2	Tripeptidyl-peptidase II
yor348c	p52569	SLC7A2	Low-affinity cationic amino acid transporter-2/CAT-2	yjl084c	q03164	MLL	Zinc finger protein HRX
yor348c	p52569	SLC7A2	Low-affinity cationic amino acid transporter-2/CAT-2	Ymr228w	q01082	SPTB2	Beta-spectrin chain, brain
yor353c	p22792	CPN2	Low-affinity cationic amino acid transporter-2/CAT-2	ygr120c	p49454	CENPF	CENP-F kinetochore protein
yor353c	p35858	IGFALS	Carboxypeptidase N	ygr120c	p04114	AOB	Apolipoprotein B
yor353c	q06828	FMOD	IGF binding protein complex acid-labile	ygr120c	p30622	RSN	Restin
yor353c	p07585	DCN	Fibromodulin	yhr102w	q13177	PAK2	Serine/threonine-protein kinase PAK-gamma
yor353c	p22792	CPN2	Bone proteoglycan II [precursor]/PG40	yhr102w	q02750	PRKMK1	Dual specificity mitogen-activated protein kinase kinase 1
yor353c	p23515	OMG	Carboxypeptidase N	yhr102w	q13153	PAK1	Serine/threonine-protein kinase PAK-alpha
yor353c	p35858	IGFALS	Oligodendrocyte-myelin glycoprotein	yhr102w	q99759	MAP3K3	Mitogen-activated protein kinase kinase kinase 3
yor353c	q06828	FMOD	IGF binding protein complex acid-labile	yhr102w	p45985	MAP2K4	Dual specificity mitogen-activated protein kinase kinase 4
yor353c	q14392	GARP	Fibromodulin	yhr102w	q13163	MAP2K5	Dual specificity mitogen-activated protein kinase kinase 5
yor353c	q99102	MUC4	Garp protein/Garpin	yhr102w	p51955	NEK2	Serine/threonine-protein kinase NEK2
yor362c	p25786	PSMA1	Tracheo-bronchial mucin 4/mucin 4 [fragment]	yjl017c	p08578	SNRPE	Small nuclear ribonucleoprotein E/snRNP-E
yor375c	p00367	GLUD1	Proteasome subunit C2.	yjl124c	p14678	SNRPB	Small nuclear ribonucleoprotein associated proteins B and B'
yor375c	p49448	GLUD2	Glutamate dehydrogenase 1	yjl124c	p14648	SNRPN	Small nuclear ribonucleoprotein associated protein N
yp1049c	p51825	MLLT2	Glutamate dehydrogenase 2	ydr480w	p17931	LGALS3	Galectin-3/IgE-binding protein
yp1059w	p35754	GLRX	AF-4 protein	yil105c	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID
yp1140c	p45985	MAP2K4	Glutaredoxin.	ynl047c	q99418	ARNO	ARF nucleotide-binding site opener/ARNO protein/ARF exchange factor
			Glutaredoxin.	yhr030c	q15759	MAPK11	Mitogen-activated protein kinase 11
			Dual specificity mitogen-activated protein kinase kinase 4				

ypl140c	p46734	MAP2K3	Dual specificity mitogen-activated protein kinase kinase 3/MAP kinase kinase 3	yhr030c	p53778	MAPK12	Mitogen-activated protein kinase 12/ERK6/extracellular signal-regulated kinase 6
ypl140c	p52564	MAP2K6	Dual specificity mitogen-activated protein kinase kinase 6	yhr030c	p27361	MAPK3	Mitogen-activated protein kinase 3/extracellular signal-regulated kinase 1
ypl140c	q02750	PRKMK1	Dual specificity mitogen-activated protein kinase kinase 1	yhr030c	q13164	MAPK7	Mitogen-activated protein kinase 7/ERK5
ypl140c	q13163	MAP2K5	Dual specificity mitogen-activated protein kinase kinase 5	yhr030c	q16539	MAPK14	Mitogen-activated protein kinase 14/CSBP
ypl140c	q99759	MAP3K3	Mitogen-activated protein kinase kinase kinase 3/MEK kinase 3	yhr030c	p28482	MAPK1	Mitogen-activated protein kinase 1/extracellular signal-regulated kinase 2
ypl151c	p35806	COPP	Beta subunit of coatomer complex	yor036w	q02224	CENPE	Centromeric protein E/CENP-E protein
ypl151c	p43034	PAFAH1B1	Platelet-activating factor acetylhydrolase IB alpha subunit	yor036w	p49454	CENPF	CENP-F kinetochore protein
ypl151c	q15542	TAF2D	Transcription initiation factor TFIID 100 Kd subunit/TAFII-100	yor036w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
ypl174c	p49454	CENPF	CENP-F kinetochore protein	yhr129c	p42024	ACTR1A	Alpha-centractin
ypl174c	q02224	CENPE	Centromeric protein E/CENP-E protein	yhr129c	p42025	ACTR1B	Beta-centractin
ypl174c	p11055	MYH3	Embryonic myosin heavy chain.	yhl144w	p11055	MYH3	Embryonic myosin heavy chain.
ypl174c	p12882	MYSS	Myosin heavy chain skeletal muscle, light meromyosin region	yhl144w	p30622	RSN	Reslin
ypl174c	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform	yhl144w	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform
ypl174c	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	yhl144w	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform
ypl174c	p30622	RSN	Reslin	yhl144w	p35579	MYH9	Myosin heavy chain, nonmuscle type A/cellular myosin heavy chain, type A/NMMHC-A
ypl174c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	yhl144w	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
ypl174c	p49454	CENPF	CENP-F kinetochore protein	yhl144w	p49454	CENPF	CENP-F kinetochore protein
ypl174c	q02224	CENPE	Centromeric protein E/CENP-E protein	yhl144w	q02224	CENPE	Centromeric protein E/CENP-E protein
ypl174c	q14203	DCN1	Dynactin, 150 kD isoform [fragment]	yhl144w	p15924	DSP	Desmoplakin I and II
ypl174c	p11055	MYH3	Embryonic myosin heavy chain.	yflr423c	p12270	TPR	Nucleoprotein TPR
ypl174c	p12882	MYSS	Myosin heavy chain skeletal muscle, light meromyosin region	yflr423c	p11047	LAMC1	Laminin gamma-1 chain [precursor]/laminin B2 chain
ypl174c	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform	yflr423c	p30622	RSN	Reslin
ypl174c	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	yflr423c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
ypl174c	p30622	RSN	Reslin	yflr423c	p05787	KRT8	Keratin, type II cytoskeletal 8/cytokeratin 8/K8/CK8
ypl174c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	yflr423c	q15431	SYCP1	Synaptonemal complex protein 1/SCP-1 protein
ypl174c	p49454	CENPF	CENP-F kinetochore protein	yflr423c	p49454	CENPF	CENP-F kinetochore protein
ypl174c	q02224	CENPE	Centromeric protein E/CENP-E protein	yflr423c	q02224	CENPE	Centromeric protein E/CENP-E protein
ypl174c	q14203	DCN1	Dynactin, 150 kD isoform [fragment]	yflr423c	p15924	DSP	Desmoplakin I and II
ypl259c	p53677	P47B	Clathrin coat assembly protein AP47 homolog 2	ykl135c	q10567	ADTB1	Beta-adaptin 1
ypl259c	p53680	CLAPS2	Clathrin coat assembly protein AP17/clathrin coat associated protein AP17	ykl135c	p21851	CLAPB1	Beta adaptin
ypl260w	p12270	TPR	Nucleoprotein TPR	yhl144w	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform

ypr1260w	p17661	DES	Desmin	yil144w	p30622	RSN	Resin
ypr1260w	p33176	KNS1	Kinesin heavy chain	yil144w	p15924	DSP	Desmoplakin I and II
ypr1260w	p49454	CENPF	CENP-F kinetochore protein	yil144w	p49454	CENPF	CENP-F kinetochore protein
ypr1260w	q02224	CENPE	Centromeric protein E/CENP-E protein	yil144w	q02224	CENPE	Centromeric protein E/CENP-E protein
ypr1260w	q15032	KIAA0029	Hypothetical protein KIAA0029	yil144w	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
ypr1260w	q15431	SYCP1	Synaptonemal complex protein 1/SCP-1 protein	yil144w	p11055	MYH3	Myosin heavy chain, embryonic
ypr1260w	q16787	LAMA3	Laminin alpha-3 chain	yil144w	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform
ypr018w	p35241	RDX	Radixin	ybr195c	o00628	PTS2R	Peroxisomal targeting signal 2 receptor
ypr018w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular	ybr195c	p04901	GNB1	Guanine nucleotide-binding protein G(i)(G(s)(G(t)) beta subunit 1
ypr018w	p46821	MAP1B	Microtubule-associated protein 1B	ybr195c	q09028	RBAP48	Chromatin assembly factor 1 P48 subunit/retinoblastoma binding protein P48
ypr018w	q02832	BLSA	B-lymphocyte antigen/B-lymphocyte surface antigen	ybr195c	p11016	GNB2	Guanine nucleotide-binding protein beta subunit 2
ypr018w	q14203	DCTN1	Dynactin, 150 kD isoform [fragment]	ybr195c	q16576	RBBP7	Histone acetyl transferase type B subunit 2/retinoblastoma-binding protein
ypr018w	q16843	DBN1	Drebin E	ybr195c	p16520	GNB3	Guanine nucleotide-binding protein G(i)(G(s)(G(t)) beta subunit 3
ypr048w	p29475	NOS1	Nitric oxide synthase/neuronal NOS	yor355w	p42568	MLLT3	AF-9 protein
ypr048w	p35228	NOS2	Inducible nitric oxide synthase	yor355w	q14669	TRIP12	Thyroid receptor interacting protein 12/KIAA0045
ypr054w	p28482	MAPK1	Mitogen-activated protein kinase 1/extracellular signal-regulated kinase 2	yfl029c	p24941	CDK2	Cell division protein kinase 2
ypr054w	p53778	MAPK12	Mitogen-activated protein kinase 12/ERK6/extracellular signal-regulated kinase 6	yfl029c	p50613	CDK7	Cell division protein kinase 7/CAK/CDK-activating kinase
ypr054w	p53779	MAPK10	Mitogen-activated protein kinase 10	yfl029c	p49840	GSK3A	Glycogen synthase kinase-3 alpha
ypr054w	q13164	MAPK7	Mitogen-activated protein kinase 7/ERK5	yfl029c	q00526	CDK3	Cell division protein kinase 3
ypr054w	q15759	MAPK11	Mitogen-activated protein kinase 11	yfl029c	p49841	GSK3B	Glycogen synthase kinase-3 beta
ypr054w	q16539	MAPK14	Mitogen-activated protein kinase 14/CSBP	yfl029c	q00535	CDK5	Cell division protein kinase 5/TAU protein kinase II catalytic subunit/TPKII catalytic subunit
ypr105c	p07197	NEFM	Neurofilament triplet M protein/160 kD neurofilament protein/NF-M	ygl145w	p35749	MYH11	Myosin heavy chain, smooth muscle isoform/SMMHC [FRAGMENT]
ypr105c	p07197	NEFM	Neurofilament triplet M protein/160 kD neurofilament protein/NF-M	ygl153w	q03001	BPAG1	Bullous 230 kDa pemphigoid antigen 1
ypr105c	p07197	NEFM	Neurofilament triplet M protein/160 kD neurofilament protein/NF-M	ygr120c	p04114	APOB	Apolipoprotein B
ypr105c	p07197	NEFM	Neurofilament triplet M protein/160 kD neurofilament protein/NF-M	yhr060w	p25789	PSMA4	Proteasome subunit C9
ypr110c	p19387	POLR2C	DNA-directed RNA polymerase II 33Kd subunit/RPB33	yfr238w	p49454	CENPF	CENP-F kinetochore protein
ypr110c	p19387	POLR2C	DNA-directed RNA polymerase II 33Kd subunit/RPB33	ynl113w	q06481	APLP2	Amyloid-like protein 2/APPH/amyloid protein homolog
ypr119w	p14635	CCNB1	G2/mitotic-specific cyclin B1	ybr135w	p33551	CKS1	Cyclin-dependent kinases regulatory subunit 1
ypr119w	p20248	CCNA	G2/mitotic-specific cyclin A	ybr135w	p10275	AR	Androgen receptor
ypr119w	p14635	CCNB1	G2/mitotic-specific cyclin B1	ydr412w	p36777	LONN	Lon protease-like protein
ypr119w	p20248	CCNA	G2/mitotic-specific cyclin A	ydr412w	p36776	LONM	Mitochondrial LON protease homolog [precursor]

ypr119w	p14635	CCNB1	G2/mitotic-specific cyclin B1	yhr035w	q15437	SEC23B	Protein transprot protein Sec23 B isoform
ypr119w	p20248	CCNA	G2/mitotic-specific cyclin A	yhr035w	q15436	SEC23A	Protein transprot protein Sec23 A isoform
ypr119w	p14635	CCNB1	G2/mitotic-specific cyclin B1	ynl135c	q00688	FKBP3	Rapamycin-selective 25 Kd immunophilin
ypr119w	p20248	CCNA	G2/mitotic-specific cyclin A	ynl135c	p26885	FKBP2	FK506-binding protein/FKBP-13
ypr173c	q03527	PSMC1	26S protease (S4) regulatory subunit	yir025w	p14314	PRKCSH	Protein kinase C substrate, 80 kD protein, heavy chain/80K-H protein
ypr173c	q13608	PEX6	Peroxisome assembly factor-2/peroxisomal-type ATPase 1	yir025w	q14203	DCTN1	Dynactin, 150 kD isoform [fragment]
ypr185w	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	ygl180w	p22694	PRKACB	Testis-specific cAMP-dependent protein kinase catalytic subunit C-beta isoform
ypr185w	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	ygl180w	p17612	PRKACA	CAMP-dependent protein kinase catalytic subunit type alpha
ypr185w	p54252	MJD1	Machado-joseph disease protein 1	ygl180w	p54646	PRKAA2	5'-AMP-activated protein kinase, catalytic alpha-2 chain
ypr185w	q10571	MN1	Probable tumor suppressor protein MN1	ygl180w	q04759	PRKCQ	Protein kinase C-theta type
ypr185w	q93074	KIAA0192	Hypothetical protein KIAA0192	ygl180w	p27448	P78	Putative serine/threonine-protein kinase P78
ypr185w	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	ygr120c	p30622	RSN	Restin
ypr185w	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	ygr120c	p49454	CENPF	CENP-F kinetochore protein
ypr185w	p54252	MJD1	Machado-joseph disease protein 1	ygr120c	p04114	APOB	Apolipoprotein B
ypr185w	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	ygr253c	p25788	PSMA3	Proteasome subunit C8
ypr185w	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	ygr253c	p25787	PSMA2	Proteasome subunit C3
ypr185w	p54252	MJD1	Machado-joseph disease protein 1	ygr253c	p25786	PSMA1	Proteasome subunit C2
ypr185w	q10571	MN1	Probable tumor suppressor protein MN1	ygr253c	p34062	PSMA6	Proteasome iota chain/PROS-27
ypr185w	q93074	KIAA0192	Hypothetical protein KIAA0192	ygr253c	p25789	PSMA4	Proteasome subunit C9
ypr185w	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	yir423c	p15924	DSP	Desmoplakin I and II
ypr185w	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	yir423c	p49454	CENPF	CENP-F kinetochore protein
ypr185w	p54252	MJD1	Machado-joseph disease protein 1	yir423c	q02224	CENPE	Centromeric protein E/CENP-E protein
ypr185w	q10571	MN1	Probable tumor suppressor protein MN1	yir423c	p30622	RSN	Restin
ypr185w	q93074	KIAA0192	Hypothetical protein KIAA0192	yir423c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle

The human polypeptides disclosed in Table 7 are related as orthologs to yeast polypeptides that interact to form complexes according to the invention. Table 7 reflects this relationship and specifies a yeast accession number for a given human ortholog. In particular, Table 7 includes in column 1 the yeast accession number for the yeast "bait" sequence
5 corresponding to the indicated human ortholog. Columns 2-4 provide the accession number of the human ortholog, the name of the human ortholog, and a description of the human ortholog, respectively, of the yeast "bait sequence". Column 5 of Table 7 provides the yeast accession number of the yeast "prey" sequence. Columns 6-8 provide the accession number of the human ortholog, the name of the human ortholog, and a description of the human ortholog,
10 respectively, of the yeast "prey sequence".

In certain embodiments, one of the ortholog polypeptides includes a "bait" polypeptide selected from the polypeptides recited in Table 7, column 2, and the other ortholog polypeptide includes a "prey" protein selected from the polypeptides recited in Table 7, column 6. The yeast orthologs of these proteins are set out in columns 1 and 4 of Table 7,
15 respectively. In some embodiments the first and second polypeptides of the complex are the polypeptides enumerated in Table 7. In some embodiments a first polypeptide is a "bait" polypeptide and a second polypeptide is "target" polypeptide, while in other embodiments the first polypeptide is a "target" polypeptide and the second is a "bait" polypeptide. Conservative variants of either polypeptide which retain binding specificity are within the scope of the
20 invention, as are labeled forms of the complexes, as described above.

In other embodiments, the polypeptides are the binding domains of the "bait" and "prey" polypeptides listed in Table 7. A binding domain of a given first polypeptide may be any number of amino acids sufficient to specifically bind to, and complex with, the corresponding second polypeptide under conditions suitable for complex formation. A
25 binding domain may be the minimal number of amino acids required to retain binding affinity, or may be a larger fragment or derivative of the polypeptides listed in Table 7, columns 2 and 6.

In certain embodiments, the "bait" polypeptides of the ortholog complex are polypeptides categorized, for example, as a "Metabolism" protein in the MIPS database. In

some embodiments, the “prey” protein of the complex is also a “Metabolism” protein, while in other embodiments the “prey” protein is, for example, an “Unclassified” protein (*see* Table 7). Other exemplary MIPS categories include, *e.g.*, “Cell Growth/Cell Division/DNA Synthesis” proteins (*see* Table 2).

5 In a further aspect, the invention provides chimeric polypeptide complex that includes at least one yeast polypeptide and at least one human ortholog of the corresponding interacting yeast polypeptide. In one embodiment, there is provided a purified chimeric complex including a yeast “bait” polypeptide selected from the polypeptides recited in Table 7, column 1 and a human ortholog of the corresponding yeast “prey” polypeptide; the human ortholog is
10 selected from the polypeptides recited in Table 7, column 6 (while the corresponding yeast “prey” proteins are recited in column 5). For example, with reference to Table 7, first row, in one embodiment, a chimeric protein containing YAL032C and P16118 is provided (P16118 is the human ortholog of corresponding yeast “prey” protein YLR345W).

 In other embodiments, the complex contains a human ortholog of a yeast “bait”
15 protein and a yeast “prey” protein. The yeast “prey” protein is selected from the polypeptides recited in Table 7, column 5, and the human ortholog of the corresponding yeast “bait” protein is selected from the polypeptides recited in Table 7, column 2 (while the corresponding yeast “bait” proteins themselves are recited in column 1). For example, with reference to Table 7, first row, in one embodiment, a chimeric protein containing Q13573 and YLR345W is
20 provided (Q13573 is the human ortholog of corresponding yeast “bait” protein YAL032C).

 In certain embodiments the first and second polypeptides of the chimeric complex are the polypeptides recited in Table 7, columns 1 and 6, or columns 2 and 5, respectively, while in other embodiments, the polypeptides of the chimeric complex contain the polypeptides recited in Table 7. Conservative variants of either polypeptide which retain binding specificity
25 are within the scope of the invention, as are labeled forms of the chimeric complexes, and chimeric complexes of binding domains, as described above.

Chimeric Polypeptides, DNA, Vectors and Recombinant Cells

 In a further aspect, the invention provides a chimeric polypeptide that includes sequences of two interacting proteins according to the invention. The interacting proteins can
30 be, *e.g.*, the interacting protein pairs disclosed in Tables 3-7, herein. Also included are chimeric polypeptides including multimers, *i.e.*, sequences from two or more pairs of interacting proteins. An example of such a chimeric polypeptide is a polypeptide that includes

amino acid sequences from ProPair 1a and 1b, and from ProPair 2a and 2b. The chimeric polypeptide includes a region of a first protein covalently linked, *e.g.* via peptide bond, to a region of a second protein. In certain embodiments, the second protein is a species ortholog of the first protein. In some embodiments, the chimeric polypeptide contains regions of first and second proteins from yeast, where the proteins are selected from the “bait” and corresponding “prey” proteins recited in Table 3, columns 1 and 4, respectively. In other embodiments, the chimeric polypeptide contains regions of first and second human ortholog proteins, where the proteins are selected from the “bait” and corresponding “prey” proteins recited in Table 7, columns 2 and 6, respectively (the yeast orthologs of these proteins are recited in columns 1 and 5, respectively). In still other embodiments, the chimeric polypeptide contains regions of a first protein from yeast, and a second human ortholog protein, where the yeast proteins are selected from the “bait” and corresponding “prey” proteins recited in Table 7, columns 1 and 5, respectively, while the human ortholog proteins are selected from the “bait” and corresponding “prey” proteins recited in Table 7, columns 2 and 6, respectively.

In some embodiments, the chimeric polypeptide(s) of the complex include(s) six or more amino acids of a first protein covalently linked to six or more amino acids of a second protein. In other embodiments, the chimeric polypeptide includes at least one binding domain of a first or second protein.

Preferably, the chimeric polypeptide includes a region of amino acids of the first polypeptide able to bind to a second polypeptide. Alternatively, or in addition, the chimeric polypeptide includes a region of amino acids of the second polypeptide able to bind to the first polypeptide.

Nucleic acid encoding the chimeric polypeptide, as well as vectors and cells containing these nucleic acids, are within the scope of the present invention. The chimeric polypeptides can be constructed by expressing nucleic acids encoding chimeric polypeptides using recombinant methods, described above, then recovering the chimeric polypeptides, or by chemically synthesizing the chimeric polypeptides. Host-vector systems that can be used to express chimeric polypeptides include, *e.g.*: (i) mammalian cell systems which are infected with vaccinia virus, adenovirus; (ii) insect cell systems infected with baculovirus; (iii) yeast containing yeast vectors or (iv) bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. Depending upon the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

The expression of the specific proteins may be controlled by any promoter/enhancer known in the art including, *e.g.*: (i) the SV40 early promoter (see *e.g.*, Bernoist & Chambon, *Nature* 290: 304-310 (1981)); (ii) the promoter contained within the 3'-terminus long terminal repeat of Rous Sarcoma Virus (see *e.g.*, Yamamoto, *et al.*, *Cell* 22: 787-797 (1980)); (iii) the
5 Herpesvirus thymidine kinase promoter (see *e.g.*, Wagner, *et al.*, *Proc. Natl. Acad. Sci. USA* 78: 1441-1445 (1981)); (iv) the regulatory sequences of the metallothionein gene (see *e.g.*, Brinster, *et al.*, *Nature* 296: 39-42 (1982)); (v) prokaryotic expression vectors such as the β -lactamase promoter (see *e.g.*, Villa-Kamaroff, *et al.*, *Proc. Natl. Acad. Sci. USA* 75: 3727-3731 (1978)); (vi) the *tac* promoter (see *e.g.*, DeBoer, *et al.*, *Proc. Natl. Acad. Sci. USA* 80:
10 21-25 (1983)).

Plant promoter/enhancer sequences within plant expression vectors may also be utilized including, *e.g.*: (i) the nopaline synthetase promoter (see *e.g.*, Herrar-Estrella, *et al.*, *Nature* 303: 209-213 (1984)); (ii) the cauliflower mosaic virus 35S RNA promoter (see *e.g.*, Garder, *et al.*, *Nuc. Acids Res.* 9: 2871 (1981)) and (iii) the promoter of the photosynthetic
15 enzyme ribulose biphosphate carboxylase (see *e.g.*, Herrera-Estrella, *et al.*, *Nature* 310: 115-120 (1984)).

Promoter/enhancer elements from yeast and other fungi (*e.g.*, the Gal4 promoter, the alcohol dehydrogenase promoter, the phosphoglycerol kinase promoter, the alkaline phosphatase promoter), as well as the following animal transcriptional control regions, which
20 possess tissue specificity and have been used in transgenic animals, may be utilized in the production of proteins of the present invention.

Other animal transcriptional control sequences derived from animals include, *e.g.*: (i) the insulin gene control region active within pancreatic β -cells (see *e.g.*, Hanahan, *et al.*, *Nature* 315: 115-122 (1985)); (ii) the immunoglobulin gene control region active within
25 lymphoid cells (see *e.g.*, Grosschedl, *et al.*, *Cell* 38: 647-658 (1984)); (iii) the albumin gene control region active within liver (see *e.g.*, Pinckert, *et al.*, *Genes and Devel.* 1: 268-276 (1987)); (iv) the myelin basic protein gene control region active within brain oligodendrocyte cells (see *e.g.*, Readhead, *et al.*, *Cell* 48: 703-712 (1987)); and (v) the gonadotrophin-releasing hormone gene control region active within the hypothalamus (see *e.g.*, Mason, *et al.*, *Science*
30 234: 1372-1378 (1986)).

The vector may include a promoter operably-linked to nucleic acid sequences which encode a chimeric polypeptide, one or more origins of replication, and optionally, one or more selectable markers (*e.g.*, an antibiotic resistance gene). A host cell strain may be selected

which modulates the expression of chimeric sequences, or modifies/processes the expressed proteins in a desired manner. Moreover, different host cells possess characteristic and specific mechanisms for the translational and post-translational processing and modification (*e.g.*, glycosylation, phosphorylation, and the like) of expressed proteins. Appropriate cell lines or host systems may thus be chosen to ensure the desired modification and processing of the foreign protein is achieved. For example, protein expression within a bacterial system can be used to produce an unglycosylated core protein; whereas expression within mammalian cells ensures "native" glycosylation of a heterologous protein.

Antibodies Specific for Polypeptide Complexes

The invention further provides antibodies and antibody fragments (such as Fab or (Fab)₂ fragments) that bind specifically to the complexes described herein. By "specifically binds" is meant an antibody that recognizes and binds to a particular polypeptide complex of the invention, but which does not substantially recognize or bind to other molecules in a sample, or to any of the polypeptides of the complex when those polypeptides are not complexed.

For example, a purified complex, or a portion, variant, or fragment thereof, can be used as an immunogen to generate antibodies that specifically bind the complex using standard techniques for polyclonal and monoclonal antibody preparation.

A full-length polypeptide complex can be used, if desired. Alternatively, the invention provides antigenic fragments of polypeptide complexes for use as immunogens. In some embodiments, the antigenic complex fragment includes at least 6, 8, 10, 15, 20, or 30 or more amino acid residues of a polypeptide. In one embodiment, epitopes encompassed by the antigenic peptide include the binding domains of the polypeptides, or are located on the surface of the protein, *e.g.*, hydrophilic regions.

If desired, peptides containing antigenic regions can be selected using hydropathy plots showing regions of hydrophilicity and hydrophobicity. These plots may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, *Proc. Nat. Acad. Sci. USA* 78:3824-3828 (1981); Kyte and Doolittle, *J. Mol. Biol.* 157:105-142 (1982).

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as a polypeptide complex. Such antibodies include, *e.g.*, polyclonal, monoclonal, chimeric, single chain, Fab and F(ab')₂ fragments, and an Fab expression library. In specific embodiments, antibodies to human ortholog complexes.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies. For example, for the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed polypeptide complex. Alternatively, the immunogenic polypeptides or complex may be chemically synthesized, as discussed above. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, *e.g.*, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, *etc.*), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against complex can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide complex. A monoclonal antibody composition thus typically displays a single binding affinity for a particular protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular complex, or polypeptide, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, *e.g.*, the hybridoma technique (*see Kohler & Milstein, Nature 256: 495-497 (1975)*); the trioma technique; the human B-cell hybridoma technique (*see Kozbor, et al., Immunol Today 4: 72 (1983)*); and the EBV hybridoma technique to produce human monoclonal antibodies (*see Cole, et al., In: Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., (1985) pp. 77-96*). If desired, human monoclonal antibodies may be prepared by using human hybridomas (*see Cote, et al., Proc. Natl. Acad. Sci. USA 80: 2026-2030 (1983)*)

or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, In: *Monoclonal Antibodies and Cancer Therapy*, *supra*).

Methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*, *Science* 246: 1275-1281 (1989)) to allow rapid and effective identification of
5 monoclonal F_{ab} fragments with the desired specificity for the desired protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to a polypeptide or polypeptide complex may be produced by techniques known in the art including, *e.g.*: (i) an F_{(ab')₂} fragment produced by pepsin digestion
10 of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab')₂} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Chimeric and humanized monoclonal antibodies against the polypeptide complexes, or polypeptides, described herein are also within the scope of the invention, and can be produced
15 by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.*, *Science* 240: 1041-1043 (1988); Liu *et al.*, *Proc.*
20 *Nat. Acad. Sci. USA* 84: 3439-3443 (1987); Liu *et al.*, *J. Immunol.* 139: 3521-3526 (1987); Sun *et al.*, *Proc. Nat. Acad. Sci. USA* 84: 214-218 (1987); Nishimura *et al.*, *Cancer Res.* 47: 999-1005 (1987); Wood *et al.*, *Nature* 314: 446-449 (1985); Shaw *et al.*, *J. Natl. Cancer Inst.* 80: 1553-1559 (1988); Morrison, *Science* 229: 1202-1207 (1985); Oi *et al.*, *BioTechniques* 4: 214 (1986); U.S. Pat. No. 5,225,539; Jones *et al.*, *Nature* 321: 552-525 (1986); Verhoevan *et al.*, *Science* 239: 1534 (1988); and Beidler *et al.*, *J. Immunol.* 141: 4053-4060 (1988).
25

Methods for the screening of antibodies that possess the desired specificity include, *e.g.*, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. For example, selection of antibodies that are specific to a particular domain of a polypeptide complex is facilitated by generation of hybridomas that
30 bind to the complex, or fragment thereof, possessing such a domain.

In certain embodiments of the invention, antibodies specific for the polypeptide complexes described herein may be used in various methods, such as detection of complex, and identification of agents which disrupt complexes. These methods are described in more

detail, below. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

Polypeptide complex-specific, or polypeptide-specific antibodies, can also be used to isolate complexes using standard techniques, such as affinity chromatography or immunoprecipitation. Thus, the antibodies disclosed herein can facilitate the purification of specific polypeptide complexes from cells, as well as recombinantly produced complexes expressed in host cells.

Kits

In a specific embodiment, the invention provides kits containing a reagent, for example, an antibody described above, which can specifically detect a polypeptide complex, or a constituent polypeptide, described herein. Such kits can contain, for example, reaction vessels, reagents for detecting complex in sample, and reagents for development of detected complex, *e.g.* a secondary antibody coupled to a detectable marker. The label incorporated into the anti-complex, or anti-polypeptide antibody may include, *e.g.*, a chemiluminescent, enzymatic, fluorescent, colorimetric or radioactive moiety. Kits of the present invention may be employed in diagnostic and/or clinical screening assays.

Pharmaceutical Compositions

The invention further provides pharmaceutical compositions of purified complexes suitable for administration to a subject, most preferably, a human, in the treatment of disorders involving altered levels of such complexes. Such preparations include a therapeutically-effective amount of a complex, and a pharmaceutically acceptable carrier. As utilized herein, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal

or a state government or listed in the U.S. Pharmacopoeia or other generally recognized pharmacopoeia for use in animals and, more particularly, in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered and includes, but is not limited to such sterile liquids as water and oils.

5 The therapeutic amount of a complex which will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and may be determined by standard clinical techniques by those of average skill within the art. In addition, *in vitro* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of
10 administration, and the overall seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. // However, suitable dosage ranges for intravenous administration of the complexes of the present invention are generally about 20-500 micrograms (μ g) of active compound per kilogram (Kg) body weight. Suitable dosage ranges for intranasal administration are generally about 0.01
15 pg/kg body weight to 1 mg/kg body weight. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems. Suppositories generally contain active ingredient in the range of 0.5% to 10% by weight; oral formulations preferably contain 10% to 95% active ingredient.

Various delivery systems are known and can be used to administer a pharmaceutical
20 preparation of a complex of the invention including, e.g.: (i) encapsulation in liposomes, microparticles, microcapsules; (ii) recombinant cells capable of expressing the polypeptides of the complex; (iii) receptor-mediated endocytosis (*see, e.g., Wu et al., J. Biol. Chem.* 262: 4429-4432 (1987)); (iv) construction of a nucleic acid encoding the polypeptides of the complex as part of a retroviral or other vector, and the like.

25 Methods of administration include, e.g., intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The pharmaceutical preparations of the present invention may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together
30 with other biologically-active agents. Administration can be systemic or local. In addition, it may be advantageous to administer the pharmaceutical preparation into the central nervous system by any suitable route, including intraventricular and intrathecal injection. Intraventricular injection may be facilitated by an intraventricular catheter attached to a

reservoir (e.g., an Ommaya reservoir). Pulmonary administration may also be employed by use of an inhaler or nebulizer, and formulation with an aerosolizing agent. It may also be desirable to administer the pharmaceutical preparation locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation, local infusion during
5 surgery, topical application, by injection, by means of a catheter, by means of a suppository, or by means of an implant. In a specific embodiment, administration may be by direct injection at the site (or former site) of a malignant tumor or neoplastic or pre-neoplastic tissue.

Alternatively, pharmaceutical preparations of the invention may be delivered in a vesicle, in particular a liposome, (see, e.g., Langer, *Science* 249:1527-1533 (1990)) or via a
10 controlled release system including, e.g., a delivery pump (see, e.g., Saudek, *et al.*, *New Engl. J. Med.* 321: 574 (1989) and a semi-permeable polymeric material (see, e.g., Howard, *et al.*, *J. Neurosurg.* 71: 105 (1989)). Additionally, the controlled release system can be placed in proximity of the therapeutic target (e.g., the brain), thus requiring only a fraction of the systemic dose. See, e.g., Goodson, In: *Medical Applications of Controlled Release*, 1984
15 (CRC Press, Boca Raton, FL).

Screening, Diagnostic, and Therapeutic Methods

The invention further provides methods of identifying an agent which modulate formation or stability a polypeptide complex described herein. By modulate is meant to
20 increase or decrease the rate at which the complex is assembled or disassembled, or to increase or decrease the stability of an assembled complex. Thus, an agent can be tested for its ability to disrupt a complex, or to promote formation or stability of a complex.

In one embodiment, the invention provides a method of identifying an agent that promotes disruption of a complex. The method includes providing a polypeptide complex,
25 contacting the complex with a test agent, and detecting the presence of a polypeptide displaced from the complex. The presence of displaced polypeptide indicates the disruption of the complex by the agent. In some embodiments, the complex is a human ortholog complex, as described above, which includes "bait" and "prey" proteins selected from those recited in Table 7. In other embodiments, the complex contains at least one microtubule or
30 microtubule-associated protein, as described above, and is selected from the complexes recited in Table 4. In other embodiments, the complex contains at least one heme biosynthesis protein, as described above, and is the complex recited in Table 5. In yet another embodiment, the complex contains at least one cell wall or cell wall-synthesis protein, as described above,

and is selected from the complexes recited in Table 6. Agents which disrupt complexes of the invention may present novel modulators of cell processes and pathways in which the complexes participate. For example, agents which disrupt complexes involving microtubule proteins may be selected as potential anti-fungal therapeutics.

5 Any compound or other molecule (or mixture or aggregate thereof) can be used as a test agent. In some embodiments, the agent can be a small peptide, or other small molecule produced by *e.g.*, combinatorial synthetic methods known in the art. Disruption of the complex by the test agent, *e.g.* binding of the agent to the complex, can be determined using art recognized methods, *e.g.*, detection of polypeptide using polypeptide-specific antibodies, as
10 described above. Bound agents can alternatively be identified by comparing the relative electrophoretic mobility of complexes exposed to the test agent to the mobility of complexes that have not been exposed to the test agent.

 Agents identified in the screening assays can be further tested for their ability to alter and/or modulate cellular functions, particularly those functions in which the complex has been
15 implicated. These functions include, *e.g.*, control of cell-cycle progression; regulation of transcription; control of intracellular signal transduction, etc., as described in detail above.

 In another embodiment, the invention provides methods for inhibiting the interaction of a polypeptide with a ligand, by contacting a complex of the protein and the ligand with an agent that disrupts the complex, as described above. In certain embodiments, the polypeptides
20 are microtubule or microtubule-associated proteins, heme biosynthesis proteins, or cell wall or cell wall-synthesis proteins. In certain embodiments, the ligand is an interacting polypeptide, and the polypeptide and ligands are selected from those recited in Tables 4-6. Inhibition of complex formation allows for modulation of cellular functions and pathways in which the targeted complexes participate.

25 In another embodiment, the invention provides a method for identifying a polypeptide complex in a subject. The method includes the steps of providing a biological sample from the subject, detecting, if present, the level of polypeptide complex. In some embodiments, the complex includes a first polypeptide (a "bait" polypeptide) selected from the polypeptides recited in Table 7, column 2, and a second polypeptide ("prey" polypeptide) selected from the
30 polypeptides recited in Table 7, column 6. Any suitable biological sample potentially containing the complex may be employed, *e.g.* blood, urine, cerebral-spinal fluid, plasma, etc. Complexes may be detected by, *e.g.*, using complex-specific antibodies as described above.

The method provides for diagnostic screening, including in the clinical setting, using, *e.g.*, the kits described above.

In still another embodiment, the present invention provides methods for detecting a polypeptide in a biological sample, by providing a biological sample containing the polypeptide, contacting the sample with a corresponding polypeptide to form a complex under suitable conditions, and detecting the presence of the complex. A complex will form if the sample does, indeed, contain the first polypeptide. In some embodiments, the polypeptide being detecting is a "prey" protein selected from the polypeptides recited in Table 7, column 6, and is detected by complexing with the corresponding "bait" protein recited in Table 7, column 2. Conversely, in other embodiments the polypeptide being detected is the "bait" protein. Alternatively, a yeast "bait" or "prey" ortholog may be employed to form a chimeric complex with the polypeptide in the biological sample.

In still another embodiment, the invention provides methods for removing a first polypeptide from a biological sample by contacting the biological sample with the corresponding second peptide to form a complex under conditions suitable for such formation. The complex is then removed from the sample, effectively removing the first polypeptide. As with the methods of detecting polypeptide described above, the polypeptide being removed may be either a "bait" or "prey" protein, and the second corresponding polypeptide used to remove it may be either a yeast or human ortholog polypeptide.

Methods of determining altered expression of a polypeptide in a subject, *e.g.* for diagnostic purposes, are also provided by the invention. Altered expression of proteins involved in cell processes and pathways can lead to deleterious effects in the subject. Altered expression of a polypeptide in a given pathway leads to altered formation of complexes which include the polypeptide, hence providing a means for indirect detection of the polypeptide level. The method involves providing a biological sample from a subject, measuring the level of a polypeptide complex of the invention in the sample, and comparing the level to the level of complex in a reference sample having known polypeptide expression. A higher or lower complex level in the sample versus the reference indicates altered expression of either of the polypeptides that forms the complex. The detection of altered expression of a polypeptide can be use to diagnose a given disease state, and or used to identify a subject with a predisposition for a disease state. Any suitable reference sample may be employed, but preferably the test sample and the reference sample are derived from the same medium, *e.g.* both are urine, etc.

The reference sample should be suitably representative of the level polypeptide expressed in a control population.

In a certain embodiment, the polypeptide complex contains a "bait" polypeptide selected from the polypeptides recited in Table 7, column 2, and a "prey" polypeptide selected from the polypeptides recited in Table 7, column 6.

The invention further provides methods for treating or preventing a disease or disorder involving altered levels of a polypeptide complex, or polypeptide, disclosed herein, by administering to a subject a therapeutically-effective amount of at least one molecule that modulates the function of the complex. As discussed above, altered levels of polypeptide complexes described herein may be implicated in disease states resulting from a deviation in normal function of the pathway in which a complex is implicated. For example, altered levels of the observed complex between YGR010Wp and YLR328Wp may be implicated in disruptions in arginine metabolism, leading to retinal atrophy, for example. In subjects with a deleteriously high level of complex, modulation may consist, for example, by administering an agent which disrupts the complex, or an agent which does not disrupt, but down-regulates, the functional activity of the complex. Alternatively, modulation in subjects with a deleteriously low level of complex may be achieved by pharmaceutical administration of complex, constituent polypeptide, or an agent which up-regulates the functional activity of complex. Pharmaceutical preparations suitable for administration of complex are described above.

In one embodiment, a disease or disorder involving altered levels of a polypeptide selected from the polypeptides recited in Table 7, column 2 or the corresponding polypeptides in column 4, is treated by administering a molecule that modulates the function of the polypeptide. In certain embodiments, the modulating molecule is the corresponding polypeptide, *e.g.* administering a "prey" protein corresponding to a "bait" protein modulates the latter by forming a complex with it.

The details of one or more embodiments of the invention are set forth in the description above. Although any methods and materials similar or equivalent to those described herein can be used in the practice of the present invention, the preferred methods and materials are now described. For example, additional interactions can be identified using other two-hybrid systems (*i.e.* using a LexA binding domain fusion or *HIS3* as a reporter gene), including variables such as different protein domains or genomic activation domain libraries. Other features, objects, and advantages of the invention will be apparent from the description and from the claims.

The following examples are presented in order to more fully illustrate the preferred embodiments of the invention. These examples should in no way be construed as limiting the scope of the invention, as defined by the appended claims.

5 EXAMPLE 1—CLONING OF *S. CEREVISIAE* OPEN-READING FRAMES

6144 potential yeast open-reading frames (ORFs) have been previously described. See Goffeau *et al.*, *supra*. These ORFs were amplified by PCR as full-length fragments, and each fragment was fused to sequences encoding the Gal4 DNA binding domain and the Gal4 activation domain by gap-repair cloning into the vectors pOBD2 and pOAD. PCR amplified products of the 6144 yeast ORFs were made by amplification of yeast cDNA using 70 oligonucleotide primers to allow recombination with centromeric plasmids pOBD2 and pOAD. See Hudson *et al.*, *Genome Res* 7: 1169 (1997). The yeast strains used were YULH (*MATa ura3-52 trp1 lys2 his3 leu2 gal4 gal80 GAL1-URA3 GAL1-LacZ*) for the Gal4 binding domain fusion in pOBD2 and N106r (*MATα ura3-52 his3 ade2 trp1 leu2 gal4 gal80 cyh2 lys2::GAL1-HIS3 ura3::GAL1-LacZ*) for the Gal4 AD fusion in pOAD. Yeast transformations were performed in a 96-well format using the lithium acetate procedure. See Ito *et al.*, *J. Bacteriol.* 153: 163 (1983). Five μ l from individual transformations were grown on selective media lacking leucine (Sc-Leu) or tryptophan (Sc-Trp) for two days and grown at 30°C. Patches of transformants were manually transferred into individual wells on micro-assay plates, to generate 64 barcoded 96-well plates for further use.

Of the 6144 ORFs, 5345 (87%) were successfully cloned into both plasmids (Table 1). Transformants from the Gal4 activation domain array were pooled to form an activation domain library. As yeast strains of opposite mating type were used to generate the two arrays, each binding domain fusion transformant was mated in duplicate to the activation domain library, and diploid cells that expressed interacting pairs were selected. Mating reactions were performed on 96-well filter plates (Millipore MAHV S45) by mixing 10^7 *MATa* cells (Gal4 binding domain fusion) with 5×10^6 *MATα* cells (activation domain library) from liquid cultures in complete media (YPAD). After filtration, the 96-well filter plates were incubated overnight at 30°C on rectangular YPAD solid media plates. Cells were collected from each filter with sterile water and the diploids containing potential interactors were selected on media lacking uracil and simultaneously screened by the addition of X-gal by incubating 4 days at 30°C. Each mating generated 5×10^5 to 10^6 diploids per well, and was performed in

duplicate to insure the reproducibility of the results. Up to 12 blue colonies were picked per mating and submitted for PCR and sequencing. A total of 8676 blue colonies were picked from the screen, 6909 (80%) passed PCR, sequencing, vector trimming, and annotation quality control, and 6215 (72%) passed interaction quality control.

5 To conduct transformation and mating reactions on such a large scale in a timely fashion, 96-well assay plates and a semi-automated Zymark® work station were used throughout the cloning and screening procedures. Sample handling and manipulation during the screens were tracked by computer, and data analysis was carried out using web-based software developed at CuraGen (GeneScape®). The final product of the screening process
10 was a collection of 96-well plates of diploid clones. The activation domain fusion plasmids were sequenced to identify the yeast ORF. The resulting sequences were compared to the yeast sequence database using Blast2. *See Altschul et al., J. Mol. Biol. 215: 403 (1990).* Using these results, a list of interactors was obtained, as discussed above (*see* Table 3).

 Results from this screen were also compared with a compilation of previously
15 described interactions. Thirty-one protein pairs identified in the present screen were previously reported as two-hybrid interactions, and an additional 18 pairs confirmed interactions previously identified by biochemical assays (co-immunoprecipitation, copurification, affinity column). *See MIPS Yeast Genome Database (MYGD) Functional Catalogue, supra.; Mewes et al., supra.; YPD™* information available at
20 www.proteome.com/YPDhome.html. Thus, 49 out of the 692 interactions identified in this screen overlap the approximately 700 interactions in *S. cerevisiae* reported in the literature. *See id.*

 The limited overlap between the results described herein and the literature (7%) can be attributed to specifics of the screen: the exclusive use of full-length proteins as both binding
25 and activation domain fusions and the version of the two-hybrid system used, which includes Gal4 as the binding domain fusion protein, centromeric plasmids, and a stringent reporter gene (*URA3*). Each of these components can affect the sensitivity of the assay. *See Legrain et al., Nucl. Acid. Res. 22: 3241 (1994).*

CLAIMS

WE CLAIM:

- 5 1. A purified complex comprising a first polypeptide and a second polypeptide, wherein said first polypeptide comprises an amino acid sequence of a polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 1, and wherein said second polypeptide comprises an amino acid sequence of the corresponding polypeptide recited in Table 3, column 5; or
- 10 said first polypeptide comprises an amino acid sequence of a polypeptide selected from the group consisting of the polypeptides recited in Table 7, column 2, and wherein said second polypeptide comprises the amino acid sequence of the corresponding polypeptide recited in Table 7, column 6; or
- 15 said first and second polypeptide comprise the amino acid sequences of a first polypeptide-second polypeptide selected from the group consisting of APG7-AUT7, DUO1-BIM1, BUB3-MAD3, KAR4-MUM2, CLN3-MAD3, EBS1-MAD2, MSB2-MAD2, MSB2-MAD3, NUP157-MAD2, SAP4-MAD2, SAP4-MAD3, SIN4-MAD2, SIN4-MAD3, YDR214W-MAD2, YNL218W-MAD2, MCM16-MCM22, CYP2-JSN1, SPC34-JSN1, YIL065C-JSN1, YLR392C-JSN1, SED1-HEM13, CDC11-SPR28, YFR042W-KRE6,
- 20 YDR482C-SCW11, SMI1-BAS1, and WSC3-PEX14.
2. The complex of claim 1, wherein said first polypeptide is selected from the group consisting of the polypeptides recited in Table 3, column 1, and wherein said second polypeptide is the corresponding polypeptide recited in Table 3, column 5.
- 25 3. The complex of claim 1, wherein said first polypeptide is labeled.
4. The complex of claim 1, wherein said second polypeptide is labeled.
- 30 5. The complex of claim 3, wherein said second polypeptide is labeled.
6. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 1a-128a, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting
- 35 of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 1b-128b.

7. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 129a-140a, and wherein said second polypeptide is the corresponding polypeptide selected from the group
5 consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 129b-140b.

8. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 141a-144a, and
10 wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 141b-144b.

9. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 145a-154a, and
15 wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 145b-154b.

20 10. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 155a-170a, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 155b-170b.

25 11. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 171a-177a, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair
30 171b-177b.

12. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 178a-194a, and wherein said second polypeptide is the corresponding polypeptide selected from the group

consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 178b-194b.

13. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 195a-310a, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 195b-310b.

14. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 311a-351a, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 311b-351b.

15. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 352a-367a, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 352b-367b.

16. The complex of claim 1, wherein said first polypeptide is the polypeptide recited in Table 3, column 1, which is denoted as ProPair 368a, and wherein said second polypeptide is the corresponding polypeptide recited in Table 3, column 5, which is denoted as ProPair 368b.

17. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 369a-374aa, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 369b-374b.

18. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 375a-431a, and wherein said second polypeptide is the corresponding polypeptide selected from the group

consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 375b-431b.

19. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 432a-440a, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 432b-440b.

20. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 441a-580a, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 441b-580b.

21. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 581a-692a, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 581b-692b.

22. The complex of claim 1, wherein said first and second polypeptide comprise the amino acid sequences of a first polypeptide-second polypeptide selected from the group consisting of APG7-AUT7, DUO1-BIM1, BUB3-MAD3, KAR4-MUM2, CLN3-MAD3, EBS1-MAD2, MSB2-MAD2, MSB2-MAD3, NUP157-MAD2, SAP4-MAD2, SAP4-MAD3, SIN4-MAD2, SIN4-MAD3, YDR214W-MAD2, YNL218W-MAD2, MCM16-MCM22, CYP2-JSN1, SPC34-JSN1, YIL065C-JSN1, YLR392C-JSN1, SED1-HEM13, CDC11-SPR28, YFR042W-KRE6, YDR482C-SCW11, SMI1-BAS1, and WSC3-PEX14.

23. The complex of claim 1, wherein said first polypeptide comprises an amino acid sequence of a polypeptide selected from the group consisting of the polypeptides recited in Table 7, column 2, and wherein said second polypeptide comprises the amino acid sequence of the corresponding polypeptide recited in Table 7, column 6.

24. The complex of claim 1, wherein said first polypeptide is selected from the group consisting of the polypeptides recited in Table 7, column 2, and wherein said second polypeptide is the corresponding polypeptide recited in Table 7, column 6.

5 25. A purified complex comprising a first polypeptide and a second polypeptide, wherein said first polypeptide comprises a region of amino acids of a polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 1 sufficient to allow said first polypeptide to bind said second polypeptide, and wherein said second polypeptide comprises a region of amino acids of the corresponding polypeptide recited in Table 3, column
10 5 sufficient to bind said first polypeptide.

26. A chimeric polypeptide comprising six or more amino acids of the first polypeptide of claim 1 covalently linked to six or more amino acids of the second polypeptide of claim 1.

15 27. A nucleic acid encoding the chimeric polypeptide of claim 26.

28. A vector comprising the nucleic acid of claim 27.

29. A cell comprising the vector of claim 28.

20 30. An antibody which specifically binds the complex of claim 1.

31. The antibody of claim 30, wherein said antibody binds to the complex of claim 1 with higher affinity than it binds to said first or second polypeptide when said polypeptides are not
25 complexed.

32. A pharmaceutical composition comprising the complex of claim 1.

33. A kit comprising a reagent which can specifically detect the complex of claim 1.

30 34. The kit of claim 33, wherein said reagent is selected from the group consisting of an antibody specific for said complex, an antibody specific for said first polypeptide, and an antibody specific for said second polypeptide.

35. A method of identifying an agent which disrupts a polypeptide complex, the method comprising:

- (a) providing the complex of claim 1;
 - (b) contacting the complex with a test agent; and
 - (c) detecting the presence of a polypeptide displaced from said complex,
- wherein the presence of displaced polypeptide indicates said agent disrupts said complex.

36. A method for identifying an agent which disrupts a polypeptide complex comprising at least one microtubule/microtubule-associated protein, heme biosynthesis protein, or cell wall/cell-wall synthesis protein, the method comprising:

- (a) providing the complex of claim 22;
 - (b) contacting said complex with a test agent; and
 - (c) detecting the presence of a polypeptide displaced from said complex,
- wherein the presence of displaced polypeptide indicates said agent disrupts said complex.

37. A method for inhibiting interaction of a microtubule or microtubule-associated protein, with a ligand, the method comprising:

contacting a complex comprising said protein and said ligand with an agent that disrupts said complex, wherein said complex is selected from the group consisting of APG7-AUT7, DUO1-BIM1, BUB3-MAD3, KAR4-MUM2, CLN3-MAD3, EBS1-MAD2, MSB2-MAD2, MSB2-MAD3, NUP157-MAD2, SAP4-MAD2, SAP4-MAD3, SIN4-MAD2, SIN4-MAD3, YDR214W-MAD2, YNL218W-MAD2, MCM16-MCM22, CYP2-JSN1, SPC34-JSN1, YIL065C-JSN1, and YLR392C-JSN1, thereby inhibiting interaction of said protein with said ligand.

38. A method for inhibiting interaction of a heme biosynthesis protein with a ligand, the method comprising:

contacting a complex comprising said protein and said ligand with an agent that disrupts said complex, wherein said complex comprises SED1-HEM13, thereby inhibiting interaction of said protein with said ligand.

39. A method for inhibiting interaction of a cell wall or cell wall-synthesis protein with a ligand, said method comprising the step of:

5 contacting a complex comprising said protein and said ligand with an agent that
disrupts said complex, wherein said complex is selected from the group consisting of
CDC11-SPR28, YFR042W-KRE6, YDR482C-SCW11, SMI1-BAS1, and
WSC3-PEX14,

thereby inhibiting interaction of said protein with said ligand.

10 40. A method of identifying a polypeptide complex in a subject, the method comprising:

- (a) providing a biological sample from said subject; and
 - (b) detecting, if present, the polypeptide complex of claim 1 in said sample,
- thereby identifying said complex.

15 41. A method of detecting a polypeptide in a biological sample, the method comprising:

- (a) providing a biological sample comprising the first polypeptide of claim 1;
- (b) contacting said biological sample with the second polypeptide of claim 1 under conditions suitable for formation of a complex comprising said first and second polypeptides; and

20 (c) detecting the presence of a complex of said first and second polypeptide,
wherein the presence of said complex indicates the presence of said first polypeptide in
said sample.

42. A method of detecting a polypeptide in a biological sample, the method comprising:

- 25 (a) providing a biological sample comprising the second polypeptide of claim 1;
- (b) contacting said biological sample with the first polypeptide of claim 1 under conditions suitable for formation of a complex comprising said first and second polypeptides; and
 - (c) detecting the presence of a complex of said first and second polypeptide,
- 30 wherein the presence of said complex indicates the presence of said second polypeptide
in said sample.

43. A method of removing a polypeptide from a biological sample, the method comprising:

- (a) providing a biological sample comprising the first polypeptide of claim 1;
 - (b) contacting said biological sample with the second polypeptide of claim 1 under conditions suitable for formation of a complex comprising said first and second polypeptide; and
 - (c) removing said complex from said sample,
- thereby removing said first polypeptide from said sample.

44. A method of determining altered expression of a polypeptide in a subject, the method comprising:

- (a) providing a biological sample from said subject,
 - (b) measuring the level of the complex of claim 1 in said sample; and
 - (c) comparing the level of said complex from step (b) to the level of said complex in a reference sample whose level of the complex of claim 1 is known,
- thereby determining whether said subject has altered expression of said first or second polypeptide.

45. A method of treating or preventing a disease or disorder involving altered levels of the complex of claim 1, the method comprising:

administering a therapeutically-effective amount of least one molecule that modulates the function of said complex to a subject in need thereof.

CORRECTED VERSION

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(54) Title: PROTEIN-PROTEIN FROM S. CEREVISIAE AND METHODS OF USING SAME

(57) Abstract: The invention provides complexes of at least two polypeptides from the yeast *S. cerevisiae* and methods of using the same. Purified complexes of two polypeptides are provided, including chimeric complexes, and chimeric polypeptides and complexes thereof are also provided, as are nucleic acids encoding chimeric polypeptides and vectors and cells containing the same. Also provided are methods of identifying agents that disrupt polypeptide complexes, methods of identifying complex or polypeptide in a sample, and for removing the same, methods of determining altered expression of a polypeptide in a subject and methods of treating/preventing disorders involving altered levels of complex or polypeptide.

WO 00/60066 A1

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 00/08399

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 0046406	A	10-08-2000	NONE	
WO 9935256	A	15-07-1999	AU 1778099 A	26-07-1999

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1-45

Present claims 1-45 relate to an extremely large number of possible compounds and thereon based methods. Support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT is to be found, however, for only a very small proportion of the compounds and pertinent methods claimed. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Consequently, the search has been carried out for those parts of the claims which appear to be supported and disclosed, namely those parts relating to the use of double-hybrid technique for screening of *S. cerevisiae* and thereby detected proteins. This method is not claimed per se, but is the basis of the present application. Moreover the subject matter of all claims was considered to be so speculative in scope that no more refined search was deemed to be possible.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/08399

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO 99 35256 A (INSTITUT PASTEUR & AFFIMETRIX) 15 July 1999 (1999-07-15) the whole document	1-45
P,X	--- A FLORES ET AL.: "A protein-protein interaction map of yeast RNA polymerase III" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA., vol. 96, no. 14, 6 July 1999 (1999-07-06), pages 7815-7820, XP002146712 NATIONAL ACADEMY OF SCIENCE. WASHINGTON., US ISSN: 0027-8424 cited in the application the whole document	1-45
P,X	--- P UETZ ET AL.: "A comprehensive analysis of protein-protein interactions in Saccharomyces cerevisiae" NATURE., vol. 403, 10 February 2000 (2000-02-10), pages 623-627, XP000938869 MACMILLAN JOURNALS LTD. LONDON., GB ISSN: 0028-0836 the whole document -----	1-45

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/08399

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	L WODICKA ET AL.: "Genome-wide expression monitoring in <i>Saccharomyces cerevisiae</i> " NATURE BIOTECHNOLOGY., vol. 15, no. 12, December 1997 (1997-12), pages 1359-1367, XP002100297 NATURE PUBLISHING., US ISSN: 1087-0156 the whole document	1-45
X	N LECRENIER ET AL.: "Two-hybrid systematic screening of the yeast proteome" BIOESSAYS, vol. 20, no. 1, January 1998 (1998-01), pages 1-5, XP002100659 CAMBRIDGE, GB ISSN: 0265-9247 the whole document	1-45
X	C BENDIXEN ET AL.: "A yeast mating-selection for detection of protein-protein interactions" NUCLEIC ACIDS RESEARCH., vol. 22, no. 9, 1994, pages 1778-1779, XP002004038 OXFORD UNIVERSITY PRESS, SURREY., GB ISSN: 0305-1048 the whole document	1-45
X	Y LUO ET AL.: "Cloning and analysis of DNA-binding proteins by yeast one-hybrid and one-two-hybrid systems" BIOTECHNIQUES., vol. 20, no. 4, April 1996 (1996-04), pages 564-568, XP002146710 EATON PUBLISHING, NATICK., US ISSN: 0736-6205 the whole document	1-45
X	R J CHO ET AL.: "Parallel analysis of genetic selections using whole genome oligonucleotide arrays" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA., vol. 95, no. 7, 31 March 1998 (1998-03-31), pages 3752-3757, XP002146711 NATIONAL ACADEMY OF SCIENCE. WASHINGTON., US ISSN: 0027-8424 the whole document	1-45
E	WO 00 46406 A (ALPHAGENE INC.) 10 August 2000 (2000-08-10) the whole document	1-45
	-/--	

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/08399

A. CLASSIFICATION OF SUBJECT MATTER

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According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

CHEM ABS Data, BIOSIS, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	M FROMONT-RACINE ET AL.: "Toward a functional analysis of the yeast genome through exhaustive two-hybrid screens" NATURE GENETICS., vol. 16, no. 7, 16 July 1997 (1997-07-16), pages 277-282, XP000770741 NATURE AMERICA, NEW YORK., US ISSN: 1061-4036 cited in the application the whole document --- -/--	1-45

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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